

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 06:37:03 ; Search time 163 Seconds
(without alignments)
59.319 Million cell updates/sec

Title: US-10-751-743-4

Sequence: 1 CRVTHPHLKDLYRSIAKPKRKP 25

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp19808:*
2: geneseqp19808:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	136	100.0	114	6	ABG74772 Canine Ig
2	136	100.0	115	6	ABG74774 Human IgE
3	136	100.0	117	6	ABG74773 Human IgE
4	136	100.0	124	2	AAW24097 Partial c
5	136	100.0	312	3	AAV79995 Dog Immun
6	136	100.0	346	6	ABG74781 Human IgE
7	136	100.0	347	6	ABG74783 Human CH2
8	136	100.0	348	6	ABG74782 Human CH2
9	136	100.0	417	2	AAW23067 Canine Ig
10	136	100.0	426	6	ABP96583 Dog IgE h
11	136	100.0	426	6	ABP96583 Dog IgE h
12	120.5	88.6	341	3	AAW24102 Canine im
13	115	84.6	431	8	ADG73237 Can Immun
14	115	84.6	431	8	ADG73237 Can Immun
15	115	84.6	436	6	ABP96580 Cat IgE h
16	115	84.6	436	6	ABU09338 Feline Ig
17	115	84.6	436	6	ABU09338 Feline Ig
18	115	84.6	436	6	ABU09338 Feline Ig
19	105	77.2	340	3	ABG74776 Rat IgE C
20	105	77.2	340	3	ABG74776 Rat IgE C
21	105	77.2	346	3	ABG74785 Human CH2
22	105	77.2	428	6	ABP96589 Rat IgE h
23	102	75.0	20	2	AAW24102 Canine im
24	99.5	73.2	341	3	AAW24102 Canine im
25	98	72.1	424	5	AAW50103 Equine Ig

26	98	72.1	424	5	AAW50104 Equine Ig
27	98	72.1	569	6	ABP96585 Horse IgE
28	95.5	70.2	342	3	AAW50103 Equine Ig
29	95.5	70.2	555	8	ADP90027 Opossum-h
30	95.5	70.2	555	8	ADP90027 Opossum-h
31	94	69.1	567	6	ABP96588 Pig IgE h
32	93.5	68.8	345	3	AAW50103 Equine Ig
33	91.5	67.3	353	8	ADP90031 Opossum-h
34	91.5	67.3	557	8	ADP90031 Opossum-h
35	91.5	67.3	557	8	ADP90031 Opossum-h
36	91.5	67.3	557	8	ADP90031 Opossum-h
37	91.5	67.3	557	8	ADP90031 Opossum-h
38	91.5	67.3	557	8	ADP90031 Opossum-h
39	91.5	67.3	557	8	ADP90031 Opossum-h
40	91.5	67.3	557	8	ADP90031 Opossum-h
41	91.5	67.3	557	8	ADP90031 Opossum-h
42	90.5	66.5	337	8	ADP90022 Opossum-h
43	90.5	66.5	337	8	ADP90022 Opossum-h
44	89	65.4	17	3	AAW50894 Antibody
45	89	65.4	17	3	AAW50893 Antibody

ALIGNMENTS

RESULT 1	ABG74772	standard, protein, 114 AA.
XX	ABG74772;	
AC	ABG74772;	
XX	05-JUN-2003 (first entry)	
DT	Canine IgE CH3 domain.	
XX		
XX	CH3 domain; IgE; antigen; non-anaphylactic; anti-IgE; fusion protein;	
KW	dermatological; anti-inflammatory; ophthalmological; allergy; asthma;	
KW	allergic rhinitis; gastrointestinal allergy; food allergy; eosinophilia;	
KW	conjunctivitis; glomerular nephritis; flea allergy; atopic dermatitis;	
KW	gene therapy; dog.	
XX		
OS	Canis familiaris.	
XX		
PN	EP1262491-A2.	
XX		
PD	04-DEC-2002.	
XX		
XX	22-MAY-2002; 2002BP-00253606.	
PF		
XX	22-MAY-2001; 2001US-0292638P.	
PR		
XX	(PF12) PFIZER PROD INC.	
PA		
XX	Brown TM, Morey MA;	
PI	WPI, 2003-122561/12.	
DR	N-PSDB; ACAS1170.	
XX		
XX	Novel isolated antigenic peptide comprising amino acid residues of CH3	
PT	domain of IgE molecule from first species and a second unrelated species,	
PT	induces non-anaphylactic anti-IgE immune response in animal.	
XX		
XX	Claim 15; Page 28; 50pp; English.	
PS		
XX		
XX	This invention describes a novel antigenic peptide comprising amino acid	
CC	residues of an IgE CH3 domain from a first species (ADB1) and amino acid	
CC	residues of an IgE CH3 domain of a second unrelated species (ADB2), where	
CC	ADB1 is conserved in the IgE CH3 domain of the first species and ADB2 is	
CC	not conserved in the IgE CH3 domain of the second species. The novel	
CC	antigenic peptide induces a non-anaphylactic anti-IgE immune response in	
CC	an animal. The invention also discloses the polynucleotide sequence	
CC	encoding the antigenic peptide and an antigenic fusion protein comprising	
CC	the antigenic peptide of the invention and a heterologous protein	

Query Match	100.0%	Score 136	DB 6	Length 114
Best Local Similarity	100.0%	Pred. No. 6	Se-13	
Matches	25	Conservative	0	Mismatches 0
Indels	0	Gaps	0	
QY	1	CRVTHPHLPKDIVRSIAAPGKRAP	25	
Db	89	CRVTHPHLPKDIVRSIAAPGKRAP	113	

RESULT 2	
ABG74774	
ID	ABG74774 standard; protein; 115 AA.
YV	

DT	23-OCT-2003	(revised)
DT	05-JUN-2003	(first entry)

human IgB CH3 domain-canine CH3 domain chimeric construct.

gene therapy; glomerular nephritis; flea allergy; atopic dermatitis; conjunctivitis; gastrointestinal allergy; food allergy; eosinophilia; allergic rhinitis; dermatological; antinflammatory; ophthalmological; allergy; asthma; allergic rhinitis; antigen; non-anaphylactic; anti-IGE; fusion protein; dermatology; IGE; antigen; non-anaphylactic; anti-IGE; fusion protein; gene therapy; glomerular nephritis; flea allergy; atopic dermatitis; conjunctivitis; gastrointestinal allergy; food allergy; eosinophilia; allergic rhinitis; dermatological; antinflammatory; ophthalmological; allergy; asthma; allergic rhinitis; antigen; non-anaphylactic; anti-IGE; fusion protein; dermatology; IGE; antigen; non-anaphylactic; anti-IGE; fusion protein;

OS Homo sapiens.
OS Canis familiaris.
OS Chimeric.

PF 22-MAY-2002; 2002EP-00253606.
RX
RR 22-MAY-2001; 2001US-0292638P.
XX
XX
(PFIZ) PFIZER PROD INC.
VA

I Brown TM, Morseby MA,
 X
 R WPI, 2003-122561/12.
 R N-PSDB; ACAA5172.

Claim 2, Page 29-30, 50pp; English

50 Sequence 115 AA;

1 This invention describes a novel antigenic peptide comprising amino acid
2 residues of an IgB CH3 domain from a first species (ADB1) and amino acid
3 residues of an IgB CH3 domain of a second unrelated species (ADB2), where
4 ADB1 is conserved in the IGE CH3 domain of the second species and ADB2 is
5 not conserved in the IgB CH3 domain of the first species. The novel
6 antigenic peptide induces a non-anaphylactic anti-IgE immune response in
7 an animal. The invention also discloses the polynucleotide sequence
8 encoding the antigenic peptide and an antigenic fusion protein comprising
9 the antigenic peptide of the invention and a heterologous protein
10 carrier, where the fusion protein induces an anti-IgE immune response
11 that does not cause anaphylaxis when administered to an animal. The
12 products of the invention have dermatological, antiinflammatory and
13 ophthalmological activity. The antigenic peptide described is capable of
14 preventing IgE from binding to high affinity receptors on mast cells and
15 basophils. The products of the invention are useful in the manufacture of
16 a medicament for treating or preventing IgE-mediated allergic disorders
17 including asthma, allergic rhinitis, gastrointestinal allergies such as
18 food allergies or atopic dermatitis, in an animal, e.g. human or dog. The
19 polynucleotide products are useful for treating IgE-mediated allergic
20 disorders, by gene therapy. Antigenic peptides comprising conserved amino
21 acid residues of the CH3 domain of an IgB molecule from one species
22 flanked by variable amino acid residues of the CH3 domain of an IgB
23 molecule from a second unrelated species are capable of inducing a high
24 titre of anti-IgB antibodies when administered to an animal without
25 causing anaphylaxis. ABG74772-ABG74785 represents polypeptide sequences
26 used in designing the constructs described in the disclosure of the
27 invention. (Updated on 23-OCT-2003 to standardise OS field)

Query Match	100.0%	Score 136,	DB 6,	Length 115,
Best Local Similarity	100.0%	Pred. No. 6,	6e-13,	
Matches	25;	Conservative	0;	Mismatches 0;
Qy	1	CRVTHPHLPKDIVRSIAAPGKRAP	25	
Db	90	CRVTHPHLPKDIVRSIAAPGKRAP	114	

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RESULT 3
ABG74773
ID   ABG74773 standard; protein; 117 AA
xx

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DT 05-JUN-2003 (first entry)

Human IgE CH3 domain fusion construct.

KW dermatological; anti-*tig*; antigen; non-anaphylactic; anti-*tge*; fusion protein;
allergic rhinitis; gastrointestinal allergy; ophthalmological; allergy; asthma;
conjunctivitis; glomerular nephritis; food allergy; eosinophilia;
gene therapy; human; dog.

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OS Homo sapiens.
OS Canis familiaris.
OS Synthetic.

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PN	EPI262491-A2.
XX	
PD	04-DEC-2002.
XX	
PF	22-MAY-2002; 2002EP-00253606

PR 22-MAY-2001; 2001US-0292638P.
PR
XX
PA (PFIZ) PFIZER PROD INC.
...

PI Brown TM, Morse MA,
XX
DR WPI; 2003-122561/12.

DR N-PSDB; ACA55171.
 XX Novel isolated antigenic peptide comprising amino acid residues of CH3
 PT domain of Igs molecule from first species and a second unrelated species,
 XX induces non-anaphylactic anti-IgE immune response in animal.
 PS Claim 2; Page 29; 50pp; English.
 CC This invention describes a novel antigenic peptide comprising amino acid
 CC residues of an Igs CH3 domain from a first species (ADEx1) and amino acid
 CC residues of an Igs CH3 domain of a second unrelated species (ADEx2), where
 CC ADEx1 is conserved in the Igs CH3 domain of the second species and ADEx2 is
 CC not conserved in the Igs CH3 domain of the first species. The novel
 CC antigenic peptide induces a non-anaphylactic anti-IgE immune response in
 CC an animal. The invention also discloses the polynucleotide sequence
 CC encoding the antigenic peptide and an antigenic fusion protein comprising
 CC the antigenic peptide of the invention and a heterologous protein
 CC carrier, where the fusion protein induces an anti-IgE immune response
 CC that does not cause anaphylaxis when administered to an animal. The
 CC products of the invention have dermatological, antiinflammatory and
 CC ophthalmological activity. The antigenic peptide described is capable of
 CC preventing Igs from binding to high affinity receptors on mast cells and
 CC basophils. The products of the invention are useful in the manufacture of
 CC a medicament for treating or preventing Igs-mediated allergic disorders
 CC including asthma, allergic rhinitis, gastrointestinal allergies such as
 CC food allergies, eosinophilia, conjunctivitis, glomerular nephritis, flea
 CC allergies or atopic dermatitis, in an animal, e.g. human or dog. The
 CC polynucleotide products are useful for treating Igs-mediated allergic
 CC disorders, by gene therapy. Antigenic peptides comprising conserved amino
 CC acid residues of the CH3 domain of an Igs molecule from one species
 CC flanked by variable amino acid residues of the CH3 domain of an Igs
 CC molecule from a second unrelated species are capable of inducing a high
 CC titre of anti-IgE antibodies when administered to an animal without
 CC causing anaphylaxis. ABG74772-ABG74785 represents polypeptide sequences
 CC used in designing the constructs described in the disclosure of the
 CC invention
 CC
 CC
 SO Sequence 117 AA,
 Query Match 100.0%; Score 136; DB 6; Length 117;
 Best Local Similarity 100.0%; Pred. No. 6.7e-13;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRVTHPLPKDVIYRSIAKAPGRAP 25
 DB 92 CRVTHPLPKDVIYRSIAKAPGRAP 116
 RESULT 4
 AAW24097
 ID AAW24097 standard; peptide; 124 AA.
 XX
 AC AAW24097;
 XX
 DT 21-NOV-1997. (first entry)
 XX
 DE Partial canine immunoglobulin E protein.
 XX
 KM Immunoglobulin E; Igs; anti-canine Igs antibody; allergy; canine; dog.
 XX
 OS Canis familiaris.
 XX
 PN JP09169795-A.
 XX
 PD 30-JUN-1997.
 XX
 PF 22-DEC-1995; 95JP-00334381.
 XX
 PR 22-DEC-1995; 95JP-00334381.
 XX
 PA (HITB) HITACHI CHEM CO LTD.
 XX
 DR WPI, 1997-389423/36.

DR N-PSDB; AAT85646.
 XX Canine immunoglobulin E peptide fragment and related DNA - useful for the
 PT preparation of anti-canine immunoglobulin E antibody.
 XX
 PS Claim 1; Page 8; 12pp; Japanese.
 CC This is a partial canine immunoglobulin E (Igs) protein. Peptide
 CC fragments (AAW24098-106) containing at least five continuous amino acids
 CC of this sequence are used for the preparation of anti-canine Igs
 CC antibody. The anti-canine Igs antibody can be used for the diagnosis of
 CC canine allergies
 CC
 CC
 SO Sequence 124 AA,
 Query Match 100.0%; Score 136; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 7.2e-13;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRVTHPLPKDVIYRSIAKAPGRAP 25
 DB 62 CRVTHPLPKDVIYRSIAKAPGRAP 86
 RESULT 5
 AAY79995
 ID AAY79995 standard; protein; 312 AA.
 XX
 AC AAY79995;
 XX
 DT 15-MAY-2000 (first entry)
 XX
 DE Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.
 XX
 KM Immunoglobulin E; Igs; epsilon heavy chain; antigenic; antigen;
 KM immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KM antibody; allergy; allergic disease; immunisation; anti-allergic;
 KM anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
 XX
 OS Canis sp.
 XX
 PN WO967293-A1.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US013959.
 XX
 PR 20-JUN-1998; 98US-00100287.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY, Walfield AM;
 XX
 DR WPI; 2000-160578/14.
 XX
 PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy.
 XX
 PS Example 1; Page 66-68; 155pp; English.
 CC The present invention describes immunoglobulin E (Igs)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for
 CC a target effector site on the epsilon-heavy chain of Igs, and so
 CC preventing triggering and activation of mast cells and basophils and
 CC downregulation of Igs synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against Igs-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic

CC constraints (disulfide bridge) to stabilize conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe (non-
 CC anaphylactogenic) antibodies. AY879994 to AY880084 represent amino acid
 CC sequences used in the exemplification of the present invention
 XX

Sequence 312 AA;

Query Match 100.0%; Score 136; DB 3; Length 312;
 Best Local Similarity 100.0%; Pred. No. 2e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIVRSIAKAPGKRAP 25
 DB 192 CRVTHPHLPKDIVRSIAKAPGKRAP 216

RESULT 6
 ABG74781 100.0%; Score 136; DB 3; Length 312;
 Best Local Similarity 100.0%; Pred. No. 2e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ABG74781; 192 CRVTHPHLPKDIVRSIAKAPGKRAP 216

05-JUN-2003 (first entry)

Human IGB CH2-canine CH3-human CH4 IGE-1 fusion protein.

CH3 domain; IGB; antigen; non-anaphylactic; anti-IGE; fusion protein;
 dermatological; anti-inflammatory; ophthalmological; allergy; asthma;
 allergic rhinitis; gastrointestinal allergy; food allergy; eosinophilia;
 conjunctivitis; glomerular nephritis; flea allergy; atopic dermatitis;
 gene therapy; human; canine; dog.

Homo sapiens.
 Canis familiaris.

EP1262491-A2.

04-DEC-2002.

22-MAY-2002; 2002EP-00253606.

22-MAY-2001; 2001US-0292638P.

(PFIZ) PRIZER PROD INC.

Brown TM, Morsey MA;

WPI; 2003-122561/12.

N-PSDB; ACA55179.

Novel isolated antigenic peptide comprising amino acid residues of CH3
 domain of IGB molecule from first species and a second unrelated species,
 induces non-anaphylactic anti-IGE immune response in animal.

Claim 3; Page 34-36; 50pp; English.

This invention describes a novel antigenic peptide comprising amino acid
 residues of an IGB CH3 domain from a first species (ADB1) and amino acid
 residues of an IGB CH3 domain of a second unrelated species (ADB2), where
 ADB1 is conserved in the IGB CH3 domain of the second species and ADB2 is
 not conserved in the IGB CH3 domain of the first species. The novel
 antigenic peptide induces a non-anaphylactic anti-IGE immune response in
 an animal. The invention also discloses the polynucleotide sequence
 encoding the antigenic peptide and an antigenic fusion protein comprising
 the antigenic peptide of the invention and a heterologous protein
 carrier, where the fusion protein induces an anti-IGE immune response
 that does not cause anaphylaxis when administered to an animal. The
 products of the invention have dermatological, anti-inflammatory and
 ophthalmological activity. The antigenic peptide described is capable of
 preventing IGB from binding to high affinity receptors on mast cells and
 basophils. The products of the invention are useful in the manufacture of
 a medicament for treating or preventing IGB-mediated allergic disorders
 including asthma, allergic rhinitis, gastrointestinal allergies such as

CC food allergies, eosinophilia, conjunctivitis, glomerular nephritis, flea
 CC allergies or atopic dermatitis, in an animal, e.g. human or dog. The
 CC polynucleotide products are useful for treating IGB-mediated allergic
 CC disorders, by gene therapy. Antigenic peptides comprising conserved amino
 CC acid residues of the CH3 domain of an IGB molecule from one species
 CC flanked by variable amino acid residues of the CH3 domain of an IGB
 CC molecule from a second unrelated species are capable of inducing a high
 CC titre of anti-IGE antibodies when administered to an animal without
 CC causing anaphylaxis. ABG74772-ABG74785 represents polypeptide sequences
 CC used in designing the constructs described in the disclosure of the
 CC invention

Sequence 346 AA;

Query Match 100.0%; Score 136; DB 6; Length 346;
 Best Local Similarity 100.0%; Pred. No. 2.3e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIVRSIAKAPGKRAP 25
 DB 217 CRVTHPHLPKDIVRSIAKAPGKRAP 241

ABG74783 100.0%; Score 136; DB 6; Length 346;
 Best Local Similarity 100.0%; Pred. No. 2.3e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ABG74783; 217 CRVTHPHLPKDIVRSIAKAPGKRAP 241

05-JUN-2003 (first entry)

Human CH2-human/canine CH3-human CH4 IGE-3 fusion protein.

CH3 domain; IGB; antigen; non-anaphylactic; anti-IGE; fusion protein;
 dermatological; anti-inflammatory; ophthalmological; allergy; asthma;
 allergic rhinitis; gastrointestinal allergy; food allergy; eosinophilia;
 conjunctivitis; glomerular nephritis; flea allergy; atopic dermatitis;
 gene therapy; human; canine; dog.

Homo sapiens.
 Canis familiaris.

EP1262491-A2.

04-DEC-2002.

22-MAY-2002; 2002EP-00253606.

22-MAY-2001; 2001US-0292638P.

(PFIZ) PRIZER PROD INC.

Brown TM, Morsey MA;

WPI; 2003-122561/12.

N-PSDB; ACA55181.

Novel isolated antigenic peptide comprising amino acid residues of CH3
 domain of IGB molecule from first species and a second unrelated species,
 induces non-anaphylactic anti-IGE immune response in animal.

Claim 3; Page 37-39; 50pp; English.

This invention describes a novel antigenic peptide comprising amino acid
 residues of an IGB CH3 domain from a first species (ADB1) and amino acid
 residues of an IGB CH3 domain of a second unrelated species (ADB2), where
 ADB1 is conserved in the IGB CH3 domain of the second species and ADB2 is
 not conserved in the IGB CH3 domain of the first species. The novel
 antigenic peptide induces a non-anaphylactic anti-IGE immune response in
 an animal. The invention also discloses the polynucleotide sequence
 encoding the antigenic peptide and an antigenic fusion protein comprising
 the antigenic peptide of the invention and a heterologous protein
 carrier, where the fusion protein induces an anti-IGE immune response

CC that does not cause anaphylaxis when administered to an animal. The
CC products of the invention have dermatological, anti-inflammatory and
CC ophthalmological activity. The antigenic peptide described is capable of
CC preventing Igs from binding to high affinity receptors on mast cells and
CC basophils. The products of the invention are useful in the manufacture of
CC a medicament for treating or preventing Igs-mediated allergic disorders
CC including asthma, allergic rhinitis, gastrointestinal allergies such as
CC food allergies, eosinophilia, conjunctivitis, glomerular nephritis, flea
CC allergies or atopic dermatitis, in an animal, e.g. human or dog. The
CC polynucleotide products are useful for treating Igs-mediated allergic
CC disorders, by gene therapy. Antigenic peptides comprising conserved amino
CC acid residues of the CH3 domain of an Igs molecule from one species
CC flanked by variable amino acid residues of the CH3 domain of an Igs
CC molecule from a second unrelated species are capable of inducing a high
CC titre of anti-Igs antibodies when administered to an animal without
CC causing anaphylaxis. ABG74772-ABG74785 represents polypeptide sequences
CC used in designing the constructs described in the disclosure of the
CC invention

SO Sequence 347 AA,
Query Match 100.0%; Score 136; DB 6; Length 347;
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIYRSIAKAPGKRAP 25
DB 218 CRVTHPLPKDIYRSIAKAPGKRAP 242

RESULT 8
ABG74782
XX ABG74782;
XX
DT 05-JUN-2003 (first entry)
XX
DE Human CH2-human/canine CH3-human CH4 Igs-2 fusion protein.
XX
XX CH3 domain; Igs; antigen; non-anaphylactic; anti-Igs; fusion protein;
XX dermatological; anti-inflammatory; ophthalmological; allergy; asthma;
XX allergic rhinitis; gastrointestinal allergy; food allergy; eosinophilia;
XX conjunctivitis; glomerular nephritis; flea allergy; atopic dermatitis;
XX gene therapy; human; canine; dog.
XX
XX Homo sapiens.
XX Canis familiaris.
XX
XX EP1262491-A2.
XX
XX PD 04-DEC-2002.
XX
XX PF 22-MAY-2002; 2002EP-00253606.
XX
XX PR 22-MAY-2001; 2001US-0292638P.
XX
XX (PF12) PFIZER PROD INC.
XX
XX Brown TM, Moresey MA;
XX
XX WPI, 2003-122561/12.
XX N-PSDB; ACAS5180.
XX
XX Novel isolated antigenic peptide comprising amino acid residues of CH3
XX domain of Igs molecule from first species and a second unrelated species,
XX induces non-anaphylactic anti-Igs immune response in animal.
XX
XX Claim 3, Page 36-37, 50pp; English.
XX
XX This invention describes a novel antigenic peptide comprising amino acid
XX residues of an Igs CH3 domain from a first species (ADBI) and amino acid
XX residues of an Igs CH3 domain of a second unrelated species (ADE2), where

CC ADE1 is conserved in the Igs CH3 domain of the second species and ADE2 is
CC not conserved in the Igs CH3 domain of the first species. The novel
CC antigenic peptide induces a non-anaphylactic anti-Igs immune response in
CC an animal. The invention also discloses the polynucleotide sequence
CC encoding the antigenic peptide and an antigenic fusion protein comprising
CC the antigenic peptide of the invention and a heterologous protein
CC carrier, where the fusion protein induces an anti-Igs immune response
CC that does not cause anaphylaxis when administered to an animal. The
CC products of the invention have dermatological, anti-inflammatory and
CC ophthalmological activity. The antigenic peptide described is capable of
CC preventing Igs from binding to high affinity receptors on mast cells and
CC basophils. The products of the invention are useful in the manufacture of
CC a medicament for treating or preventing Igs-mediated allergic disorders
CC including asthma, allergic rhinitis, gastrointestinal allergies such as
CC food allergies, eosinophilia, conjunctivitis, glomerular nephritis, flea
CC allergies or atopic dermatitis, in an animal, e.g. human or dog. The
CC polynucleotide products are useful for treating Igs-mediated allergic
CC disorders, by gene therapy. Antigenic peptides comprising conserved amino
CC acid residues of the CH3 domain of an Igs molecule from one species
CC flanked by variable amino acid residues of the CH3 domain of an Igs
CC molecule from a second unrelated species are capable of inducing a high
CC titre of anti-Igs antibodies when administered to an animal without
CC causing anaphylaxis. ABG74772-ABG74785 represents polypeptide sequences
CC used in designing the constructs described in the disclosure of the
CC invention

SO Sequence 348 AA;
Query Match 100.0%; Score 136; DB 6; Length 348;
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIYRSIAKAPGKRAP 25
DB 219 CRVTHPLPKDIYRSIAKAPGKRAP 243

RESULT 9
AAW23067
XX AAW23067 standard; protein; 417 AA.
XX
XX AAW23067;
XX
DT 19-FEB-1998 (first entry)
XX
XX Canine Igs heavy chain constant region (exon 1-4 product).
XX
XX Igs; immunoglobulin; antibody; heavy chain constant region; allergy;
XX hypersensitivity; therapy; dog; antisense; immunomodulation.
XX
XX Canis familiaris.
XX
XX
XX Key Location/Qualifiers
XX
XX MISC-difference 55
XX FT /note= "encoded by ACC"
XX FT MISC-difference 56
XX FT /note= "encoded by TAC"
XX FT MISC-difference 67
XX FT /note= "encoded by GCC"
XX FT MISC-difference 83
XX FT /note= "encoded by NMT"
XX FT MISC-difference 174
XX FT /note= "encoded by GGN"
XX FT MISC-difference 175
XX FT /note= "encoded by NNG"
XX FT MISC-difference 176
XX FT /note= "encoded by TGN"
XX FT MISC-difference 203
XX FT /note= "encoded by TCC"
XX FT MISC-difference 204
XX FT /note= "encoded by GAC"
XX
XX MO9730156-A2.

XX 21-AUG-1997.
PD 14-FEB-1997; 97WO-US002322.
XX 14-FEB-1996; 96US-00601197.
XX (INDEX-) IDEXX LAB INC.
XX Mermer B, Harris RA, Siefring AB;
PI WPI; 1997-425031/39.
DR N-PSDB; AAT79278.
XX Isolated canine IGE heavy chain constant region DNA - useful to develop
PT products for treatment of canine allergies and for immunomodulation in
PT dogs.
XX Disclosure; Page 35-39; 59pp; English.
PS This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IGE
CC heavy chain constant region (epsilon) genomic DNA. Another polypeptide,
CC comprising the exon 5 and 6 product, is given in AAW23068. Recombinant
CC peptides encoded by exons 1-6 can be produced in eukaryotic or
CC prokaryotic cells. Such peptides, and antibodies raised against them, are
CC used in methods to treat the manifestation of allergy in dogs, e.g. to
CC treatment Type I immediate hypersensitivity, and for immunomodulation
XX Sequence 417 AA;
SQ

Query Match 100.0%; Score 136; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 2, 8e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIVRSIAKAPGKRAP 25
DB 289 CRVTHPHLPKDIVRSIAKAPGKRAP 313

RESULT 10
AAR97753 ID AAR97753 standard; protein; 426 AA.
XX AAR97753;
AC AAR97753;
XX 28-AUG-1996 (first entry)
DT 28-AUG-1996 (first entry)
XX Canine IGE.
DE IGE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.
KM IGE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.
XX Canis familiaris.
OS WO9614867-A1.
XX WO9614867-A1.
XX 23-MAY-1996.
PD 23-MAY-1996.
XX 03-NOV-1995; 95WO-US013795.
PF 03-NOV-1995; 95WO-US013795.
XX 09-NOV-1994; 94US-00336583.
PR 09-NOV-1994; 94US-00336583.
XX (MERI) MERCK & CO INC.
PA (MERI) MERCK & CO INC.
XX Hollis GF, Patel MD;
PI WPI; 1996-277321/28.
DR N-PSDB; AAT29824.
XX New DNA encoding canine IGE and IGA - useful in vaccines, anti-sense
PT therapy, assays, drug screening, etc.
XX Claim 11; Page 29-30; 49pp; English.
PS

XX The canine IGE amino acid sequence (AAR97753) was deduced from an
CC isolated gene (AAT29824) obtd. from a canine liver DNA library. The
CC cloning of the IGE gene allows prodn. of large quantities of recombinant
CC IGE using bacterial, yeast, mammalian, insect or viral systems. The IGE
CC can be used in drug development (e.g. small molecule screening, assay
CC development and anti-IGE antibody generation). Fragments of IGE can be
CC used in vaccines or to prevent IGE-mediated hypersensitivity. The new
CC sequence information permits targeted modulation of IGE-mediated immune
CC response
XX Sequence 426 AA;
SQ

Query Match 100.0%; Score 136; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 2, 9e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIVRSIAKAPGKRAP 25
DB 294 CRVTHPHLPKDIVRSIAKAPGKRAP 318

RESULT 11
ABP96583 ID ABP96583 standard; protein; 426 AA.
XX ABP96583;
AC ABP96583;
XX 28-MAY-2003 (first entry)
DT 28-MAY-2003 (first entry)
XX

DE Dog IGE heavy chain amino acid sequence SEQ ID NO:28.
XX Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;
XX immune response; major histocompatibility complex; MHC; immunogenic;
XX antiallergic; antiaesthetic; immunosuppressive; vasotropic; cytostatic;
XX dermatological; antiinflammatory; IGE-mediated condition; food allergy;
XX atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
XX atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
XX urticaria hives.

OS Canis familiaris.
XX WO2003015716-A2.
XX WO2003015716-A2.
XX 27-FEB-2003.
PD 27-FEB-2003.
XX 08-AUG-2002; 2002WO-US026986.
PF 08-AUG-2002; 2002WO-US026986.
XX 13-AUG-2001; 2001US-0312120P.
PR 13-AUG-2001; 2001US-0312120P.
XX (IGET-) IGE THERAPEUTICS INC.
PA (IGET-) IGE THERAPEUTICS INC.
XX Chen SA, Yang Y, Barankiewicz T, Chen Z;
PI WPI; 2003-268242/26.
DR WPI; 2003-268242/26.
XX

PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
PT against IGE. By identifying peptide eliciting CTL response to IGE
PT peptides naturally presented by major histocompatibility complex class I
PT protein.
XX Example 7; Page 152-154; 187pp; English.
PS

XX The present invention describes a method (M1) for identifying peptides
CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
CC E (IGE), comprising providing a test peptide (T) suspected of being able
CC to bind to major histocompatibility complex (MHC) class I molecule, and
CC evaluating (T) for ability to elicit in a mammal a CTL response to
CC naturally processed and presented IGE peptides, where a peptide that
CC induces such a response is identified. Also described are compositions:
CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
CC (C2) comprising at least one isolated polynucleotide encoding (I); and
CC (C3) comprising antigen-presenting cells that recognise at least one (I).

CC Where C1-3 are able to bind to at least one MHC class I molecule and to
 CC elicit in a mammal a CTL response to naturally processed and presented
 CC IGE peptides. C1-3 have antiallergic, antitachymatic, immunosuppressive,
 CC vasoactive, dermatological, antiinflammatory and cytostatic activities,
 CC and can be used as inducers of a CTL response against IGE, and in
 CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a
 CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as
 CC IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic
 CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are
 CC useful for treating atopic hypersensitivity conditions (such as allergic
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
 CC hives). The present sequence represents an IGE heavy chain amino acid
 CC sequence, which is given in an example from the present invention
 XX

SO Sequence 426 AA;

Query Match 100.0%; Score 136; DB 6; Length 426;
 Best Local Similarity 100.0%; Pred. No. 2, 9e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDVIYSIAKAPGRAP 25
 DB 294 CRVTHPLPKDVIYSIAKAPGRAP 318

RESULT 12
 AAB06208
 ID AAB06208 standard; protein; 341 AA.
 XX
 AC AAB06208;
 XX
 DT 12-SEP-2003 (revised)
 DT 22-NOV-2000 (first entry)
 XX
 DE Immunogenic peptide consisting of opossum CH2, dog CH3 and opossum CH4.
 XX
 KM Dog; opossum; immunoglobulin B; IGE; vaccination; infection; allergy;
 KM asthma; eczema; immunogenic peptide.
 XX
 OS Didelphis virginiana.
 OS Canis sp.
 OS Chimeric.
 XX
 PN WO200025722-A2.
 XX
 PD 11-MAY-2000.
 XX
 PF 21-OCT-1999; 99WO-SR001896.
 XX
 PR 02-NOV-1998; 98US-0106652P.
 PR 22-SEP-1999; 99US-00401636.
 XX
 PA (RESI-) RESISTENTIA PHARM AB.
 XX
 PI Hellman LT;
 XX
 DR WPI; 2000-365342/31.
 XX
 PT Immunogenic polypeptides useful for preventing the harmful effects of
 PT immunoglobulin B in mammals.
 XX
 PS Disclosure, Fig 2; 50pp; English.
 XX
 CC The present sequence is an immunogenic peptide consisting of the heavy
 CC chain constant regions 2 and 4 of the opossum IGE and the heavy chain
 CC constant region 3 from the dog. It was shown to cause a stronger
 CC polyclonal anti-self IGE response than peptides consisting of the same
 CC regions from one mammal. Immunogenic peptides, particularly those
 CC consisting of different heavy chain constant regions, can be used for
 CC vaccination in humans, against bacterial and viral infections and
 CC allergies, such as asthma, fur, pollen and food allergies and eczema.
 CC (Updated on 12-SEP-2003 to standardise OS field)

XX
 SO Sequence 341 AA;

Query Match 88.6%; Score 120.5; DB 3; Length 341;
 Best Local Similarity 92.3%; Pred. No. 5, 7e-10;
 Matches 24; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRVTHPLPKDVIYSIAKAPGRAP 25
 DB 211 CRVTHPLPKDVIYSIAKAPGRAP 236

RESULT 13
 ADG73237
 ID ADG73237 standard; protein; 431 AA.
 XX
 AC ADG73237;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Cat immunoglobulin B (IGB) constant region.
 XX
 KM antiallergic; IGE-modulator; vaccine; feline; IGE; immunoglobulin B;
 KM immune response; IGE-mediated response; allergy; cat; constant region.
 XX
 OS Felis catus.
 XX
 PN US2003216565-A1.
 XX
 PD 20-NOV-2003.
 XX
 PF 07-APR-2003; 2003US-00409772.
 XX
 PR 07-JAN-1999; 99US-0115033P.
 PR 07-JAN-2000; 2000US-00479614.
 XX
 PA (MCCA/) MCCA/C.
 PA (WEBER/) WEBER B.
 XX
 PI Mccall C, Weber B;
 XX
 DR WPI; 2004-010802/01.
 DR N-PADB; ADG73236.
 XX
 PT New isolated nucleic acid molecule encoding a portion of a feline IGE
 PT heavy chain protein, useful for treating and/or eliciting feline immune
 PT responses for IGE-mediated responses, such as allergies.
 XX
 PS Claim 12; SEQ ID NO 14; 44pp; English.
 XX
 CC The invention describes an isolated nucleic acid molecule (I) encoding a
 CC portion of a feline IGE heavy chain protein. The methods and compositions
 CC of the present invention are useful for eliciting feline immune responses
 CC for and/or treating IGE-mediated responses, such as allergies. This is
 CC the amino acid sequence of a cat immunoglobulin B (IGB) constant region.
 XX

SO Sequence 431 AA;

Query Match 84.6%; Score 115; DB 8; Length 431;
 Best Local Similarity 84.0%; Pred. No. 5, 3e-09;
 Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDVIYSIAKAPGRAP 25
 DB 299 CRVTHPLPKDVIYSIAKAPGRAP 323

RESULT 14
 ABP96580
 ID ABP96580 standard; protein; 496 AA.
 XX
 AC ABP96580;
 XX

DT 28-MAY-2003 (first entry)
 XX Cat IGE heavy chain amino acid sequence SEQ ID NO:25.
 DE
 XX
 XX Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;
 KM immune response; major histocompatibility complex; MHC; immunogenic;
 KM antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;
 KM dermatological; antiinflammatory; IGE-mediated condition; food allergy;
 KM atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
 KM atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
 KM urticaria hives.
 XX
 XX Felis catus.
 OS
 XX MO2003015716-A2.
 PN
 XX 27-FEB-2003.
 PD
 XX 08-AUG-2002; 2002MO-US026986.
 PF
 XX 13-AUG-2001; 2001US-0312120P.
 PR
 XX (IGET-) IGE THERAPEUTICS INC.
 PA
 XX Chen SA, Yang Y, Barankiewicz T, Chen Z;
 PI
 XX WPI; 2003-268242/26.
 DR
 XX
 PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
 PT against IGE, by identifying peptide eliciting CTL response to IGE
 PT peptides naturally presented by major histocompatibility complex class I
 PT protein.
 PS
 XX Example 7; Page 145-147; 187pp; English.
 CC The present invention describes a method (M1) for identifying peptides
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
 CC E (IGE), comprising providing a test peptide (T) suspected of being able
 CC to bind to major histocompatibility complex (MHC) class I molecule, and
 CC evaluating (T) for ability to elicit in a mammal a CTL response to
 CC naturally processed and presented IGE peptides, where a peptide that
 CC induces such a response is identified. Also described are compositions:
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and
 CC (C3) comprising antigen-presenting cells that recognise at least one (I).
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to
 CC elicit in a mammal a CTL response to naturally processed and presented
 CC IGE peptides, C1-3 have antiallergic, antiasthmatic, immunosuppressive,
 CC vasotropic, dermatological, antiinflammatory and cytostatic activities,
 CC and can be used as inducers of a CTL response against IGE, and in
 CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a
 CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as
 CC IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic
 CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are
 CC useful for treating atopic hypersensitivity conditions (such as allergic
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
 CC atopic hypersensitivity conditions (such as anaphylaxis), and urticaria
 CC hives). The present sequence represents an IGE heavy chain amino acid
 CC sequence, which is given in an example from the present invention
 XX
 XX Sequence 496 AA;
 SQ
 Query Match 84.6%; Score 115; DB 6; Length 496;
 Best Local Similarity 84.0%; Pred. No. 6.2e-09;
 Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

ID ABU09338 standard; protein; 496 AA.
 XX
 XX AC ABU09338;
 XX
 XX DT 27-JUN-2003 (first entry)
 XX
 XX DE Feline IGE epsilon heavy chain #2.
 KM
 KM Feline; immunoglobulin E; IGE epsilon heavy chain; parasitic infection;
 KM IGE-mediated immune response; allergy; neoplasia; vaccine technology;
 KM antibody technology; antiallergic; antiparasitic; cytostatic.
 XX
 XX Felis catus.
 OS
 XX US2003013183-A1.
 PN
 XX 16-JAN-2003.
 PD
 XX 07-JAN-2000; 2000US-00479614.
 PF
 XX 07-JAN-1999; 99US-0115033P.
 PR
 XX (MCCA/) MCCALL C.
 PA (WEBER/) WEBER E.
 XX
 XX McCall C, Weber E;
 PI
 XX WPI; 2003-391997/37.
 DR
 XX N-PSDB; ABX95715.
 DR
 XX
 PT New nucleic acid molecule encoding feline immunoglobulin E (IGE) heavy or
 PT light chain protein, useful for treating feline IGE-mediated responses
 PT e.g. allergies, parasitic infections or neoplasia.
 PS
 XX Claim 1; Page 37-39; 45pp; English.
 CC
 CC The present invention relates to the isolation of feline immunoglobulin E
 CC (IGE) kappa light chain and IGE epsilon heavy chain proteins, and the
 CC polynucleotide sequences encoding them. The sequences of the invention
 CC are useful for treating feline IGE-mediated immune responses (e.g.
 CC allergies, parasitic infections or neoplasia), in vaccine technology,
 CC small molecule/antibody technology, molecular biology, and various
 CC immunological techniques related to feline IGE and its functions. The
 CC present sequence represents feline IGE epsilon heavy chain #2
 XX
 XX Sequence 496 AA;
 SQ
 Query Match 84.6%; Score 115; DB 6; Length 496;
 Best Local Similarity 84.0%; Pred. No. 6.2e-09;
 Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Search completed: February 22, 2005, 06:57:14
 Job time : 165 secs

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OM protein - protein search, using sw model

Run on: February 22, 2005, 06:50:48 / Search time 42 Seconds
(without alignments)
44.434 Million cell updates/sec

Title: US-10-751-743-4

Perfect score: 136
Sequence: 1 CRVTHPLPDIYRSIAKAPGKRAP 25

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	136	100.0	312	4	US-09-701-623C-2
2	136	100.0	426	1	US-08-336-583-2
3	136	100.0	426	5	PCT-US95-13795-2
4	115	84.6	71	4	US-09-281-760B-39
5	115	84.6	107	4	US-09-281-760B-36
6	115	84.6	431	4	US-09-479-614-14
7	115	84.6	436	4	US-09-479-614-2
8	115	84.6	436	4	US-09-479-614-29
9	89	65.4	17	4	US-09-281-760B-26
10	89	65.4	25	4	US-09-701-623C-6
11	89	65.4	45	4	US-09-701-623C-26
12	89	65.4	45	4	US-09-701-623C-90
13	89	65.4	46	4	US-09-701-623C-27
14	89	65.4	57	4	US-09-701-623C-88
15	89	65.4	62	4	US-09-701-623C-87
16	89	65.4	63	4	US-09-701-623C-91
17	88	64.7	313	4	US-09-701-623C-3
18	86	63.2	325	4	US-09-701-623C-1
19	78	57.4	106	2	US-08-232-539D-54
20	78	57.4	109	3	US-08-466-163B-1
21	78	57.4	109	4	US-09-802-096-1
22	78	57.4	109	4	US-09-802-077-1
23	78	57.4	113	2	US-08-232-539D-56
24	72	52.9	17	4	US-09-281-760B-28
25	72	52.9	313	4	US-09-701-623C-4
26	69	50.7	17	4	US-09-281-760B-27
27	69	50.7	33	4	US-09-701-623C-44

28	68	50.0	25	4	US-09-701-623C-7	Sequence 7, App1
29	67.5	49.6	118	3	US-08-466-151-1	Sequence 1, App1
30	67.5	49.6	119	2	US-08-466-025A-1	Sequence 1, App1
31	65	47.8	17	4	US-09-281-760B-30	Sequence 30, App1
32	64	47.1	25	3	US-09-100-414B-95	Sequence 95, App1
33	64	47.1	25	3	US-09-303-323-95	Sequence 95, App1
34	64	47.1	25	4	US-09-770-014-95	Sequence 95, App1
35	64	47.1	25	4	US-09-701-588C-92	Sequence 95, App1
36	64	47.1	25	4	US-09-701-623C-5	Sequence 5, App1
37	64	47.1	42	3	US-09-100-414B-98	Sequence 98, App1
38	64	47.1	42	3	US-09-100-414B-99	Sequence 98, App1
39	64	47.1	42	3	US-09-100-414B-100	Sequence 100, App1
40	64	47.1	42	3	US-09-303-323-98	Sequence 98, App1
41	64	47.1	42	3	US-09-303-323-99	Sequence 99, App1
42	64	47.1	42	3	US-09-303-323-100	Sequence 100, App1
43	64	47.1	42	4	US-09-770-014-98	Sequence 98, App1
44	64	47.1	42	4	US-09-770-014-99	Sequence 99, App1
45	64	47.1	42	4	US-09-770-014-100	Sequence 100, App1

ALIGNMENTS

```
RESULT 1
US-09-701-623C-2
; Sequence 2, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang Ph.D., Chang Y1
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; TITLE OF INVENTION: ALLERGY
; FILE REFERENCE: 11514153U51
; CURRENT APPLICATION NUMBER: US/09/701,623C
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURES:
; OTHER INFORMATION: CH2CH3n of dog IgE
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-09-701-623C-2
Query Match 100.0%; Score 136; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 2.7e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 CRVTHPLPDIYRSIAKAPGKRAP 25
Db 192 CRVTHPLPDIYRSIAKAPGKRAP 216
RESULT 2
US-08-336-583-2
; Sequence 2, Application US/08336583
; Patent No. 5629415
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN B
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
```

ADDRESSER: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,583
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-583-2

Query Match 100.0%; Score 136; DB 1; Length 426;
Best Local Similarity 100.0%; Pred. No. 3.9e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSIAKAPGRAP 25
DB 294 CRVTHPLPKDIVRSIAKAPGRAP 318

RESULT 3
PCT-US95-13795-2
Sequence 2, Application PC/TUS9513795
GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY P.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13795
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-13795-2

Query Match 100.0%; Score 136; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 3.9e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSIAKAPGRAP 25
DB 294 CRVTHPLPKDIVRSIAKAPGRAP 318

RESULT 4
US-09-281-760E-39
Sequence 39, Application US/09281760E
Patent No. 6734287
GENERAL INFORMATION:
APPLICANT: Lawton, Robert
APPLICANT: Mermer, Brian
APPLICANT: Francoeur, Greg
TITLE OF INVENTION: Specific Binding Protein for Treating
FILE REFERENCE: 01-1275A
CURRENT APPLICATION NUMBER: US/09/281,760E
CURRENT FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: 09/058,331
PRIOR FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 39
LENGTH: 71
TYPE: PRT
ORGANISM: Canis familiaris
US-09-281-760E-39

Query Match 84.6%; Score 115; DB 4; Length 71;
Best Local Similarity 100.0%; Pred. No. 9.4e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSIAKAPG 21
DB 51 CRVTHPLPKDIVRSIAKAPG 71

RESULT 5
US-09-281-760E-36
Sequence 36, Application US/09281760E
Patent No. 6734287
GENERAL INFORMATION:
APPLICANT: Lawton, Robert
APPLICANT: Mermer, Brian
APPLICANT: Francoeur, Greg
TITLE OF INVENTION: Specific Binding Protein for Treating
FILE REFERENCE: 01-1275A
CURRENT APPLICATION NUMBER: US/09/281,760E
CURRENT FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: 09/058,331
PRIOR FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 36
LENGTH: 107
TYPE: PRT
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: misc feature
LOCATION: (136)-(136)
OTHER INFORMATION: "n" stands for any nucleic acid

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FEATURE:
NAME/KEY: misc_feature
LOCATION: (413)..(414)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (451)..(451)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (460)..(462)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (500)..(500)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (530)..(530)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (568)..(568)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (847)..(849)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (853)..(853)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1832)..(1832)
OTHER INFORMATION: "n" stands for any nucleic acid
US-09-281-760E-36
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Query Match      84.6%; Score 115; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 CRVTHPLPDIIVRSIAKAPG 21
Db      87 CRVTHPLPDIIVRSIAKAPG 107
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RESULT 6
US-09-479-614-14
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin B Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; EARLIER FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14
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Query Match      84.6%; Score 115; DB 4; Length 431;
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Best Local Similarity 84.0%; Pred. No. 7.7e-10;
Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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```
Qy      1 CRVTHPLPDIIVRSIAKAPGKRAP 25
Db      299 CKVTHPDLPDIIVRSIAKAPGRRFP 323
```

```
RESULT 7
US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin B Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; EARLIER FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2
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Query Match      84.6%; Score 115; DB 4; Length 496;
Best Local Similarity 84.0%; Pred. No. 9.1e-10;
Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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```
Qy      1 CRVTHPLPDIIVRSIAKAPGKRAP 25
Db      364 CKVTHPDLPDIIVRSIAKAPGRRFP 388
```

```
RESULT 8
US-09-479-614-29
; Sequence 29, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin B Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; EARLIER FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29
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```
Query Match      84.6%; Score 115; DB 4; Length 496;
Best Local Similarity 84.0%; Pred. No. 9.1e-10;
Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1 CRVTHPLPDIIVRSIAKAPGKRAP 25
Db      364 CKVTHPDLPDIIVRSIAKAPGRRFP 388
```

```
RESULT 9
US-09-281-760E-26
; Sequence 26, Application US/09281760E
; Patent No. 6734287
; GENERAL INFORMATION:
```

```
/ APPLICANT: Lawton, Robert
/ APPLICANT: Merceur, Brian
/ APPLICANT: Francoeur, Greg
/ TITLE OF INVENTION: Specific Binding Protein for Treating
/ TITLE OF INVENTION: Canine Allergy
/ FILE REFERENCE: 01-1275A
/ CURRENT APPLICATION NUMBER: US/09/281,760E
/ PRIOR FILING DATE: 1999-03-30
/ PRIOR APPLICATION NUMBER: 09/058,331
/ PRIOR FILING DATE: 1998-04-09
/ NUMBER OF SEQ ID NOS: 39
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 26
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Canis familiaris
US-09-281-760E-26
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Query Match      65.4%; Score 89; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 CRVTHPLPKDIVRSI 16
Db      2 CRVTHPLPKDIVRSI 17
```

```
RESULT 10
US-09-701-623C-6
/ Sequence 6, Application US/09701623C
/ Patent No. 6811782
/ GENERAL INFORMATION:
/ APPLICANT: Wang Ph.D., Chang Yi
/ TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
/ FILE REFERENCE: 11514153US1
/ CURRENT APPLICATION NUMBER: US/09/701,623C
/ PRIOR FILING DATE: 2000-12-01
/ PRIOR APPLICATION NUMBER: PCT/US99/13959
/ PRIOR FILING DATE: 1999-06-21
/ PRIOR APPLICATION NUMBER: 09/100,287
/ PRIOR FILING DATE: 1998-06-20
/ NUMBER OF SEQ ID NOS: 91
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 25
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-701-623C-6
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Query Match      65.4%; Score 89; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 RVTTHPLPKDIVRSIAK 18
Db      8 RVTTHPLPKDIVRSIAK 24
```

```
RESULT 11
US-09-701-623C-26
/ Sequence 26, Application US/09701623C
/ Patent No. 6811782
/ GENERAL INFORMATION:
/ APPLICANT: Wang Ph.D., Chang Yi
/ TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
/ FILE REFERENCE: 11514153US1
/ CURRENT APPLICATION NUMBER: US/09/701,623C
/ PRIOR FILING DATE: 2000-12-01
/ PRIOR APPLICATION NUMBER: PCT/US99/13959
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/ PRIOR FILING DATE: 1999-06-21
/ PRIOR APPLICATION NUMBER: 09/100,287
/ PRIOR FILING DATE: 1998-06-20
/ NUMBER OF SEQ ID NOS: 91
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 26
/ LENGTH: 45
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-701-623C-26
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Query Match      65.4%; Score 89; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      2 RVTTHPLPKDIVRSIAK 18
Db      28 RVTTHPLPKDIVRSIAK 44
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```
RESULT 12
US-09-701-623C-90
/ Sequence 90, Application US/09701623C
/ Patent No. 6811782
/ GENERAL INFORMATION:
/ APPLICANT: Wang Ph.D., Chang Yi
/ TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
/ FILE REFERENCE: 11514153US1
/ CURRENT APPLICATION NUMBER: US/09/701,623C
/ PRIOR FILING DATE: 2000-12-01
/ PRIOR APPLICATION NUMBER: PCT/US99/13959
/ PRIOR FILING DATE: 1999-06-21
/ PRIOR APPLICATION NUMBER: 09/100,287
/ PRIOR FILING DATE: 1998-06-20
/ NUMBER OF SEQ ID NOS: 91
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 90
/ LENGTH: 45
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-701-623C-90
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```
Query Match      65.4%; Score 89; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      2 RVTTHPLPKDIVRSIAK 18
Db      28 RVTTHPLPKDIVRSIAK 44
```

```
RESULT 13
US-09-701-623C-27
/ Sequence 27, Application US/09701623C
/ Patent No. 6811782
/ GENERAL INFORMATION:
/ APPLICANT: Wang Ph.D., Chang Yi
/ TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
/ FILE REFERENCE: 11514153US1
/ CURRENT APPLICATION NUMBER: US/09/701,623C
/ PRIOR FILING DATE: 2000-12-01
/ PRIOR APPLICATION NUMBER: PCT/US99/13959
/ PRIOR FILING DATE: 1999-06-21
/ PRIOR APPLICATION NUMBER: 09/100,287
/ PRIOR FILING DATE: 1998-06-20
/ NUMBER OF SEQ ID NOS: 91
/ SOFTWARE: PatentIn Ver. 2.1
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SEQ ID NO 27
LENGTH: 46
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: I, M, L
NAME/KEY: MOD_RES
LOCATION: (2)
OTHER INFORMATION: S, T
NAME/KEY: MOD_RES
LOCATION: (7)
OTHER INFORMATION: K, L
NAME/KEY: MOD_RES
LOCATION: (8)
OTHER INFORMATION: G, R
NAME/KEY: MOD_RES
LOCATION: (9)
OTHER INFORMATION: V, T
NAME/KEY: MOD_RES
LOCATION: (10)
OTHER INFORMATION: I, V
NAME/KEY: MOD_RES
LOCATION: (14)
OTHER INFORMATION: I, T
NAME/KEY: MOD_RES
LOCATION: (15)
OTHER INFORMATION: E, R
NAME/KEY: MOD_RES
LOCATION: (16)
OTHER INFORMATION: G, M
NAME/KEY: MOD_RES
LOCATION: (19)
OTHER INFORMATION: F, T
NAME/KEY: MOD_RES
LOCATION: (20)
OTHER INFORMATION: G, M
US-09-701-623C-27

Query Match          65.4%; Score 89; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 6.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RVTHPHLPKDIVRSIAK 18
DB      29 RVTHPHLPKDIVRSIAK 45

RESULT 14
US-09-701-623C-88
Sequence 88, Application US/09701623C
Patent No. 6811782
GENERAL INFORMATION:
APPLICANT: Wang Ph.D., Chang Y1
TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
FILE REFERENCE: 11514153US1
CURRENT APPLICATION NUMBER: US/09/701,623C
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US99/13959
PRIOR FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: 09/100,287
PRIOR FILING DATE: 1998-06-20
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 88
LENGTH: 57
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
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US-09-701-623C-88

Query Match          65.4%; Score 89; DB 4; Length 57;
Best Local Similarity 100.0%; Pred. No. 8.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RVTHPHLPKDIVRSIAK 18
DB      40 RVTHPHLPKDIVRSIAK 56

RESULT 15
US-09-701-623C-87
Sequence 87, Application US/09701623C
Patent No. 6811782
GENERAL INFORMATION:
APPLICANT: Wang Ph.D., Chang Y1
TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
FILE REFERENCE: 11514153US1
CURRENT APPLICATION NUMBER: US/09/701,623C
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US99/13959
PRIOR FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: 09/100,287
PRIOR FILING DATE: 1998-06-20
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 87
LENGTH: 62
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-701-623C-87

Query Match          65.4%; Score 89; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 9.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RVTHPHLPKDIVRSIAK 18
DB      45 RVTHPHLPKDIVRSIAK 61

Search completed: February 22, 2005, 07:01:02
Job time : 43 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 07:00:24 ; Search time 131 Seconds

(Without alignments)
62.451 Million cell updates/sec

Title: US-10-751-743-4

Perfect score: 136
Sequence: 1 CRVTHPLPDIVRSIAKAPGKRAP 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep:*
- 3: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/prodata/2/pubppa/US06_PUBCOMB.pep:*
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- 13: /cgn2_6/prodata/2/pubppa/US10_PUBCOMB.pep:*
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- 20: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	136	100.0	25	US-09-938-700-4
2	136	100.0	114	US-10-152-190-1
3	136	100.0	115	US-10-152-190-3
4	136	100.0	117	US-10-152-190-2
5	136	100.0	346	US-10-152-190-10
6	136	100.0	347	US-10-152-190-12
7	136	100.0	348	US-10-152-190-11
8	136	100.0	426	US-10-214-524-28
9	120.5	88.6	341	US-09-401-636-11
10	120.5	88.6	341	US-10-176-664-11
11	120.5	88.6	341	US-10-673-594-11
12	115	84.6	431	US-09-479-614-14
13	115	84.6	431	US-10-409-772-14

14	115	84.6	496	10	US-09-479-614-2	Sequence 2, Appl
15	115	84.6	496	10	US-09-479-614-29	Sequence 29, Appl
16	115	84.6	496	14	US-10-214-524-25	Sequence 25, Appl
17	115	84.6	496	15	US-10-409-772-2	Sequence 2, Appl
18	115	84.6	496	15	US-10-409-772-29	Sequence 29, Appl
19	105	77.2	114	14	US-10-152-190-5	Sequence 5, Appl
20	105	77.2	340	9	US-09-401-636-2	Sequence 2, Appl
21	105	77.2	340	14	US-10-176-664-2	Sequence 2, Appl
22	105	77.2	340	15	US-10-673-594-2	Sequence 2, Appl
23	105	77.2	346	14	US-10-152-190-14	Sequence 14, Appl
24	105	77.2	428	14	US-10-214-524-34	Sequence 34, Appl
25	99.5	73.2	341	9	US-09-401-636-4	Sequence 4, Appl
26	99.5	73.2	341	9	US-10-176-664-9	Sequence 9, Appl
27	99.5	73.2	341	14	US-10-176-664-4	Sequence 4, Appl
28	99.5	73.2	341	14	US-10-176-664-9	Sequence 4, Appl
29	99.5	73.2	341	15	US-10-673-594-9	Sequence 4, Appl
30	99.5	73.2	341	15	US-10-673-594-9	Sequence 9, Appl
31	98	72.1	424	16	US-10-451-078-2	Sequence 2, Appl
32	98	72.1	424	16	US-10-451-078-4	Sequence 4, Appl
33	98	72.1	569	14	US-10-214-524-30	Sequence 30, Appl
34	95.5	70.2	342	9	US-09-401-636-8	Sequence 8, Appl
35	95.5	70.2	342	14	US-10-176-664-8	Sequence 8, Appl
36	95.5	70.2	342	15	US-10-673-594-8	Sequence 8, Appl
37	95.5	70.2	555	15	US-10-438-794-8	Sequence 8, Appl
38	95.5	70.2	555	15	US-10-453-915-8	Sequence 8, Appl
39	94	69.1	567	14	US-10-214-524-33	Sequence 33, Appl
40	93.5	68.8	345	9	US-09-401-636-10	Sequence 10, Appl
41	93.5	68.8	345	14	US-10-176-664-10	Sequence 10, Appl
42	93.5	68.8	345	15	US-10-673-594-10	Sequence 10, Appl
43	91.5	67.3	353	15	US-10-453-915-21	Sequence 21, Appl
44	91.5	67.3	557	15	US-10-438-794-12	Sequence 12, Appl
45	91.5	67.3	557	15	US-10-438-794-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-938-700-4
; Sequence 4, Application US/09938700
; Patent No. US20020064525A1
; GENERAL INFORMATION:
; APPLICANT: Morsey, et al.
; TITLE OF INVENTION: Anti-IGB Vaccines
; FILE REFERENCE: PCT0761A
; CURRENT APPLICATION NUMBER: US/09/938,700
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: PRT
; ORGANISM: DOG CH3/CH4 PEPTIDE SEQUENCE
US-09-938-700-4

Query Match 100.0%; Score 136; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 4, 6e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPLPDIVRSIAKAPGKRAP 25
DB 1 CRVTHPLPDIVRSIAKAPGKRAP 25

RESULT 2
US-10-152-190-1
; Sequence 1, Application US/10152190
; Publication No. US20030096369A1
; GENERAL INFORMATION:
; APPLICANT: Morsey, Mohamad A.
; TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IGB vaccines
; FILE REFERENCE: PCT01011A
; CURRENT APPLICATION NUMBER: US/10/152,190


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/ CURRENT FILING DATE: 2002-05-21
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 1
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Dog CH3 domain
US-10-152-190-1
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Query Match          100.0%; Score 136; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CRVTHPHLPKDIYRSIAKAPGKRAP 25
Db 89 CRVTHPHLPKDIYRSIAKAPGKRAP 113
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RESULT 3
US-10-152-190-3
/ Sequence 3, Application US/10152190
/ Publication No. US20030096369A1
/ GENERAL INFORMATION:
/ APPLICANT: Morsey, Mohamed A.
/ TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IGF vaccines
/ FILE REFERENCE: PC11011A
/ CURRENT APPLICATION NUMBER: US/10/152,190
/ CURRENT FILING DATE: 2002-05-21
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 3
/ LENGTH: 115
/ TYPE: PRT
/ ORGANISM: Human CH3/dog CH3 domain chimera
US-10-152-190-3
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Query Match          100.0%; Score 136; DB 14; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CRVTHPHLPKDIYRSIAKAPGKRAP 25
Db 90 CRVTHPHLPKDIYRSIAKAPGKRAP 114
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RESULT 4
US-10-152-190-2
/ Sequence 2, Application US/10152190
/ Publication No. US20030096369A1
/ GENERAL INFORMATION:
/ APPLICANT: Morsey, Mohamed A.
/ TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IGF vaccines
/ FILE REFERENCE: PC11011A
/ CURRENT APPLICATION NUMBER: US/10/152,190
/ CURRENT FILING DATE: 2002-05-21
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 2
/ LENGTH: 117
/ TYPE: PRT
/ ORGANISM: Human CH3/dog CH3 domain fusion
US-10-152-190-2
```

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Query Match          100.0%; Score 136; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CRVTHPHLPKDIYRSIAKAPGKRAP 25
Db 92 CRVTHPHLPKDIYRSIAKAPGKRAP 116
```

RESULT 5

```
US-10-152-190-10
/ Sequence 10, Application US/10152190
/ Publication No. US20030096369A1
/ GENERAL INFORMATION:
/ APPLICANT: Morsey, Mohamed A.
/ TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IGF vaccines
/ FILE REFERENCE: PC11011A
/ CURRENT APPLICATION NUMBER: US/10/152,190
/ CURRENT FILING DATE: 2002-05-21
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 10
/ LENGTH: 346
/ TYPE: PRT
/ ORGANISM: IGF-1 fusion protein
US-10-152-190-10
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Query Match          100.0%; Score 136; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 8.4e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CRVTHPHLPKDIYRSIAKAPGKRAP 25
Db 217 CRVTHPHLPKDIYRSIAKAPGKRAP 241
```

```
RESULT 6
US-10-152-190-12
/ Sequence 12, Application US/10152190
/ Publication No. US20030096369A1
/ GENERAL INFORMATION:
/ APPLICANT: Morsey, Mohamed A.
/ TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IGF vaccines
/ FILE REFERENCE: PC11011A
/ CURRENT APPLICATION NUMBER: US/10/152,190
/ CURRENT FILING DATE: 2002-05-21
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 12
/ LENGTH: 347
/ TYPE: PRT
/ ORGANISM: IGF-3 fusion protein
US-10-152-190-12
```

```
Query Match          100.0%; Score 136; DB 14; Length 347;
Best Local Similarity 100.0%; Pred. No. 8.5e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 CRVTHPHLPKDIYRSIAKAPGKRAP 25
Db 218 CRVTHPHLPKDIYRSIAKAPGKRAP 242
```

```
RESULT 7
US-10-152-190-11
/ Sequence 11, Application US/10152190
/ Publication No. US20030096369A1
/ GENERAL INFORMATION:
/ APPLICANT: Morsey, Mohamed A.
/ TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IGF vaccines
/ FILE REFERENCE: PC11011A
/ CURRENT APPLICATION NUMBER: US/10/152,190
/ CURRENT FILING DATE: 2002-05-21
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 11
/ LENGTH: 348
/ TYPE: PRT
/ ORGANISM: IGF-2 fusion protein
US-10-152-190-11
```

```
Query Match          100.0%; Score 136; DB 14; Length 348;
Best Local Similarity 100.0%; Pred. No. 8.5e-11;
```

```
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRVTHPLPKDIVRSIAKAPGRAP 25
Db 219 CRVTHPLPKDIVRSIAKAPGRAP 243

RESULT 8
US-10-214-524-28
; Sequence 28, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Yang, Yong-Min
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN B VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGB-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Dog (Canis familiaris)
US-10-214-524-28

Query Match 100.0%; Score 136; DB 14; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRVTHPLPKDIVRSIAKAPGRAP 25
Db 294 CRVTHPLPKDIVRSIAKAPGRAP 318

RESULT 9
US-09-401-636-11
; Sequence 11, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-11

Query Match 88.6%; Score 120.5; DB 9; Length 341;
Best Local Similarity 92.3%; Pred. No. 1.3e-08;
Matches 24; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 1 CRVTHPLPKDIVRSIAKAPGRAP 25
Db 211 CRVTHPLPKDIVRSIAKAPGRAP 236

RESULT 10
US-10-176-664-11
; Sequence 11, Application US/10176664
```

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; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-11

Query Match 88.6%; Score 120.5; DB 14; Length 341;
Best Local Similarity 92.3%; Pred. No. 1.3e-08;
Matches 24; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 1 CRVTHPLPKDIVRSIAKAPGRAP 25
Db 211 CRVTHPLPKDIVRSIAKAPGRAP 236

RESULT 11
US-10-673-594-11
; Sequence 11, Application US/10673594
; Publication No. US2004007625A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/673,594
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-673-594-11

Query Match 88.6%; Score 120.5; DB 15; Length 341;
Best Local Similarity 92.3%; Pred. No. 1.3e-08;
Matches 24; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 1 CRVTHPLPKDIVRSIAKAPGRAP 25
Db 211 CRVTHPLPKDIVRSIAKAPGRAP 236

RESULT 12
US-09-479-614-14
; Sequence 14, Application US/09479614
; Publication No. US2003003183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin B Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
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;; CURRENT FILING DATE: 2000-01-07
;; EARLIER APPLICATION NUMBER: 60/115,033
;; EARLIER FILING DATE: 1999-01-07
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 14
;; LENGTH: 431
;; TYPE: PRT
;; ORGANISM: Felis catus
US-09-479-614-14

Query Match 84.6%; Score 115; DB 10; Length 431;
Best Local Similarity 84.0%; Pred. No. 9,7e-08;
Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CRVTHPLPKDIVRSIAKAPGRAP 25
Db 299 CQVTHDPLPKDIVRSIAKAPGRRFP 323

RESULT 13

US-10-409-772-14
;; Sequence 14, Application US/10409772
;; Publication No. US20030216565A1
;; GENERAL INFORMATION:
;; APPLICANT: McCall, Catherine
;; APPLICANT: Weber, Eric
;; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
;; FILE REFERENCE: P-1047
;; CURRENT APPLICATION NUMBER: US/10/409,772
;; CURRENT FILING DATE: 2003-04-07
;; PRIOR APPLICATION NUMBER: US/09/479,614
;; PRIOR FILING DATE: 2000-01-07
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 14
;; LENGTH: 431
;; TYPE: PRT
;; ORGANISM: Felis catus
US-10-409-772-14

Query Match 84.6%; Score 115; DB 15; Length 431;
Best Local Similarity 84.0%; Pred. No. 9,7e-08;
Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CRVTHPLPKDIVRSIAKAPGRAP 25
Db 299 CQVTHDPLPKDIVRSIAKAPGRRFP 323

RESULT 14
US-09-479-614-2
;; Sequence 2, Application US/09479614
;; Publication No. US20030013183A1
;; GENERAL INFORMATION:
;; APPLICANT: McCall, Catherine
;; APPLICANT: Weber, Eric
;; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
;; FILE REFERENCE: P-1047
;; CURRENT APPLICATION NUMBER: US/09/479,614
;; CURRENT FILING DATE: 2000-01-07
;; EARLIER APPLICATION NUMBER: 60/115,033
;; EARLIER FILING DATE: 1999-01-07
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 496
;; TYPE: PRT
;; ORGANISM: Felis catus
US-09-479-614-2

Query Match 84.6%; Score 115; DB 10; Length 496;
Best Local Similarity 84.0%; Pred. No. 1,1e-07;

Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CRVTHPLPKDIVRSIAKAPGRAP 25
Db 364 CQVTHDPLPKDIVRSIAKAPGRRFP 388

RESULT 15

US-09-479-614-29
;; Sequence 29, Application US/09479614
;; Publication No. US20030013183A1
;; GENERAL INFORMATION:
;; APPLICANT: McCall, Catherine
;; APPLICANT: Weber, Eric
;; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
;; FILE REFERENCE: P-1047
;; CURRENT APPLICATION NUMBER: US/09/479,614
;; CURRENT FILING DATE: 2000-01-07
;; EARLIER APPLICATION NUMBER: 60/115,033
;; EARLIER FILING DATE: 1999-01-07
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 29
;; LENGTH: 496
;; TYPE: PRT
;; ORGANISM: Felis catus
US-09-479-614-29

Query Match 84.6%; Score 115; DB 10; Length 496;
Best Local Similarity 84.0%; Pred. No. 1,1e-07;
Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CRVTHPLPKDIVRSIAKAPGRAP 25
Db 364 CQVTHDPLPKDIVRSIAKAPGRRFP 388

Search completed: February 22, 2005, 07:14:10
Job time : 132 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 06:51:23 / Search time 38 Seconds

(without alignments)
63.301 Million cell updates/sec

Title: US-10-751-743-4

Perfect score: 136

Sequence: 1 CRVTHPHLPKDIYRSIAKGRKAP 25

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	77.2	429	1 EHRT	Ig epsilon chain C
2	89	65.4	426	2 I36948	Ig epsilon-chain C
3	86	63.2	428	1 EKHU	Ig epsilon chain C
4	80	58.8	388	1 EHM5	Ig epsilon chain C
5	80	58.8	388	2 E3864	Ig epsilon chain C
6	67	49.3	107	2 I68726	Ig epsilon chain C
7	67	49.3	107	2 I68730	Ig epsilon chain C
8	59	43.4	684	2 S60266	Ig epsilon chain C
9	58	42.6	549	2 S04845	Ig epsilon chain C
10	54	39.7	1938	1 S06005	Ig epsilon chain C
11	54	39.7	1939	2 A46762	Ig epsilon chain C
12	54	39.7	1939	2 A46762	Ig epsilon chain C
13	52	38.2	273	2 B87319	Ig epsilon chain C
14	51	37.5	572	2 B46529	Ig epsilon chain C
15	51	37.5	572	2 B46529	Ig epsilon chain C
16	51	37.5	1938	2 I49464	Ig epsilon chain C
17	51	37.5	1940	1 A24932	Ig epsilon chain C
18	51	37.5	1940	1 S04090	Ig epsilon chain C
19	50.5	37.1	277	2 I47162	Ig epsilon chain C
20	50.5	37.1	327	1 G4HU	Ig epsilon chain C
21	50.5	37.1	328	2 I47160	Ig epsilon chain C
22	50.5	37.1	328	2 I47161	Ig epsilon chain C
23	50.5	37.1	328	2 I47158	Ig epsilon chain C
24	50.5	37.1	328	2 I47159	Ig epsilon chain C
25	50.5	37.1	330	1 G2MSA	Ig epsilon chain C
26	50.5	37.1	399	1 G2MSAM	Ig epsilon chain C
27	50.5	37.1	446	2 S40295	Ig epsilon chain C
28	50.5	37.1	469	2 S37483	Ig epsilon chain C
29	50.5	37.1	538	2 A83972	Ig epsilon chain C

30	50	36.8	1038	1 MWRBCB	myosin beta heavy
31	50	36.8	1934	2 I48153	myosin beta heavy
32	50	36.8	1935	1 A37102	myosin beta heavy
33	50	36.8	1935	1 S06006	myosin beta heavy
34	50	36.8	1935	2 A59286	myosin beta heavy
35	49.5	36.4	405	1 G2MSBM	Ig epsilon chain C
36	49.5	36.4	474	1 G2MS11	Ig epsilon chain C
37	49.5	36.4	573	2 G12838	Ig epsilon chain C
38	49.5	36.0	1937	2 I38055	Ig epsilon chain C
39	49.5	36.0	1938	1 JX0178	Ig epsilon chain C
40	48.5	35.7	166	2 C72641	Ig epsilon chain C
41	48.5	35.7	234	2 PT0207	Ig epsilon chain C
42	48.5	35.7	255	4 S31866	Ig epsilon chain C
43	48.5	35.7	329	2 S00847	Ig epsilon chain C
44	48.5	35.7	330	1 G4HU	Ig epsilon chain C
45	48.5	35.7	374	2 S69339	Ig epsilon chain C

ALIGNMENTS

RESULT 1

EHRT

Ig epsilon chain C region - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 17-Dec-1982 #sequence revision 17-Dec-1982 #text_change 09-Jul-2004
C/Accession: A93442; A90937; A02143
R/Hellman, L.; Pelterson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.
Nucleic Acids Res. 10, 6041-6049, 1982
A/Title: Structure and evolution of the heavy chain from rat immunoglobulin B.
A/Reference number: A93442; PMID:83064537; PMID:6292865
A/Accession: A93442
A/Molecule type: mRNA
A/Residues: 1-429 <HL>
A/Cross-references: UNIPROT:P01855
A/Experimental source: strain I/O/c/Wsl, immunocytoma IR2
R/Kinderogel, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.
DNA 1, 335-343, 1982
A/Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction, A/Reference number: A90937; PMID:83182019; PMID:6820340
A/Accession: A90937
A/Molecule type: mRNA
A/Residues: N', 169-307, Y', 309-342 <KIN>
C/Complex: An immunoglobulin heterodimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1, C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: duplication; glycoprotein; heterodimer; immunoglobulin
P/19-80/Domain: immunoglobulin homology <IM1>
P/118-186/Domain: immunoglobulin homology <IM2>
P/223-291/Domain: immunoglobulin homology <IM3>
P/327-398/Domain: immunoglobulin homology <IM4>
P/46,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status predict.

Query Match

Best Local Similarity

Matches

1 CRVTHPHLPKDIYRSIAKGRKRA 24
289 CRVDHPKPIYRSIAKGRKRS 312

RESULT 2

I36948

Ig epsilon chain - chimpanzee (fragment)
C/Species: Pan troglodytes (chimpanzee)
C/Date: 04-Oct-1996 #sequence revision 04-Oct-1996 #text_change 21-Jan-2000
C/Accession: I36948
R/Sakoyama, Y.; Hong, K.
Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
A/Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orangutan
A/Reference number: I36948; MUID:87147196; PMID:3103123

[illegible]

1g heavy chain precursor - African clawed frog (fragment)
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 12-Feb-1993 #sequence (revision 12-Feb-1993 #text_change 26-Aug-1999
 A/Accession: S04845; S05695
 R/Mahdavi, C.T.; Haire, R.N.; Litman, G.W.
 Nucleic Acids Res. 17, 5388, 1989
 A/Title: Nucleotide sequence of a cDNA encoding a third distinct Xenopus immunoglobulin
 A/Reference number: S04845; MUID:89345103; PMID:2503814
 A/Accession: S04845
 A/Molecule type: mRNA
 A/Residues: 1-549 <AMB>
 A/Cross-references: EMBL:X15114
 R/Litman, G.W.
 submitted to the EMBL Data Library, April 1989
 A/Reference number: S05695
 A/Accession: S05695
 A/Molecule type: mRNA
 A/Residues: 'LC', 3-308, 'H', 310-549 <LIT>
 A/Cross-references: EMBL:X15114; NID:964799; PID:9763031
 C/Superfamily: immunoglobulin C region; immunoglobulin homology
 C/Keywords: glycoprotein; heterotrimer; immunoglobulin
 F/26-109/Domain: immunoglobulin homology <IMM>
 F/281,294/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 42.6%; Score 58; DB 2; Length 549;
 Best Local Similarity 52.2%; Pred. No. 1.9;
 Matches 12; Conservative 3; Mismatches 6; Indels 2; Gaps 1;
 QY 1 CRYTHRLPKDLYRSIAKA--PG 21
 DB 424 CKVHPDLPSPIKSIQKSDPG 446

RESULT 10
 S06005
 myosin alpha heavy chain, cardiac muscle [similarity] - rat
 N/Alternate names: alpha-myosin heavy chain
 N/Contains: myosin ATPase (EC 3.6.4.1)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 31-Dec-1993 #sequence (revision 31-Dec-1993 #text_change 09-Jul-2004
 A/Accession: S06005; S07535; A20971; A02988; I53305
 R/McNally, E.M.; Glanola, K.M.; Leinwand, L.A.
 Nucleic Acids Res. 17, 7527-7528, 1989
 A/Title: Complete nucleotide sequence of full length cDNA for rat alpha cardiac myosin H
 A/Reference number: S06005; MUID:90016822; PMID:2798111
 A/Accession: S06005
 A/Status: translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-1938 <MCN>
 A/Cross-references: UNIPROT:P02563; EMBL:X15938; NID:956654; PIDN:CAA34064.1; PID:956655
 R/McNally, E.M.; Kraft, R.; Bryvo-Zehnder, M.; Taylor, D.A.; Leinwand, L.A.
 J. Mol. Biol. 210, 665-671, 1989
 A/Title: Full-length rat alpha and beta cardiac myosin heavy chain sequences. Comparison
 A/Reference number: S07535; MUID:90133919; PMID:2614840
 A/Accession: S07535
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-1938 <MC2>
 R/Mahdavi, V.; Chambers, A.P.; Nadal-Ginard, B.
 Proc. Natl. Acad. Sci. U.S.A. 81, 2626-2630, 1984
 A/Title: Cardiac alpha- and beta-myosin heavy chain genes are organized in tandem.
 A/Reference number: A20971; MUID:84194059; PMID:6585819
 A/Accession: A20971
 A/Molecule type: protein
 A/Residues: 1-12, 'AP', 14-45, 'A', 47-50, 'AP', 53-81, 'E', 83-86, 'Q', 88-109, 111-133, 'H', 135-16
 Nature 297, 659-664, 1982
 A/Title: Molecular characterization of two myosin heavy chain genes expressed in the adu
 A/Reference number: A02988; MUID:8220036; PMID:7045662
 A/Accession: A02988
 A/Molecule type: mRNA
 A/Residues: 1512-1574, 'S', 1576-1721, 'N', 1723-1851, 'N', 1853-1869, 'N', 1871-1933, 'I', 1935-1
 A/Note: There are 10 or more myosin heavy chain genes in the rat, at least two of which

R/Mahdavi, V.; Lompre, A.M.; Chambers, A.P.; Nadal-Ginard, B.
 Eur. Heart J. 5, 181-191, 1984
 A/Title: Cardiac myosin heavy chain isozytic transitions during development and under p
 A/Reference number: I53305; MUID:85179510; PMID:6241892
 A/Accession: I53305
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1872-1933, 'I', 1935-1938 <RBS>
 A/Cross-references: GB:M32697; NID:9205596; PIDN:AAA1658.1; PID:9205597
 C/Superfamily: myosin heavy chain; myosin motor domain homology
 C/Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolyase; methyl
 F/87-767/Domain: myosin motor domain homology <MMOT>
 F/177-184/Region: nucleotide-binding motif A (P-loop)
 F/548-585/Region: actin binding #status predicted
 F/656-678/Region: actin binding #status predicted
 F/840-1938/Domain: coiled coil #status predicted
 F/840-1280/Region: S2
 F/1281-1938/Region: light meromyosin
 F/128/Modified site: N6; N6, N6-trimethyllysine (lys) #status predicted
 F/183/Binding site: ATP (lys) #status predicted
 F/696,706/Active site: Cys #status predicted

Query Match 39.7%; Score 54; DB 1; Length 1938;
 Best Local Similarity 50.0%; Pred. No. 26;
 Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 2 RYTHPLPKDLYRSIAKAPG 21
 DB 664 RTTHPFPVRCITPERRAPG 683

RESULT 11
 A46762
 myosin alpha heavy chain, cardiac muscle - human
 N/Contains: myosin ATPase (EC 3.6.4.1)
 C/Species: Homo sapiens (man)
 C/Date: 31-Dec-1993 #sequence (revision 31-Dec-1993 #text_change 09-Jul-2004
 A/Accession: A46762; B46762; A49354; S18830; B32562; B33835; B27858; A28908
 R/Matsuoka, K.; Beisel, K.W.; Funttani, M.; Arai, S.; Takao, A.
 Am. J. Med. Genet. 41, 537-547, 1991
 A/Title: Complete sequence of human cardiac alpha-myosin heavy chain gene and amino acid
 A/Reference number: A46762; MUID:92133665; PMID:1776652
 A/Accession: A46762
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-1939 <MAT>
 A/Cross-references: UNIPROT:P13533; UNIPROT:Q9UQV1; DBJ:DD0943; NID:9219523; PIDN:BAAO
 A/Accession: B46762
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-1461 <MA2>
 R/BP, T.A.; Dixon, I.M.C.; Wang, H.Y.; Sole, M.J.; Llew, C.C.
 Genomics 18, 508-509, 1993
 A/Title: Structural organization of the human cardiac alpha-myosin heavy chain gene (MYH
 A/Reference number: A49354; MUID:94140346; PMID:8307559
 A/Accession: A49354
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-87, 'Q', 89-573, 'Q', 575-607, 'A', 609-743, 'T', 745-789, 'W', 791-1013, 'V', 1015-10
 -1939 <RBP>
 A/Cross-references: GB:Z20656; NID:9297023; PIDN:CAA79675.1; PID:9297024
 R/Brand, N.J.; Dabnide, N.; Yacoub, M.; Barton, P.J.R.
 Biochem. Biophys. Res. Commun. 179, 1255-1258, 1991
 A/Title: Determination of the 5' exon structure of the human cardiac alpha-myosin heavy
 A/Reference number: S18830; MUID:92028859; PMID:1930170
 A/Accession: S18830
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-32 <BRA>
 A/Cross-references: EMBL:X56181; NID:9283318; PIDN:CAA39642.1; PID:9283319
 R/Yamauchi-Takahara, K.; Sole, M.J.; Llew, J.; Ing, D.; Llew, C.C.
 Proc. Natl. Acad. Sci. U.S.A. 86, 3504-3508, 1989
 A/Title: Characterization of human cardiac myosin heavy chain genes.


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A:Reference number: A94224; MUID:89264452; PMID:2726733
A:Accession: B32562
A:Molecule type: DNA
A:Residues: 1-87,'Q',89-177,1551-1732,'E',1734-1736,'T',1738-1762,'D',1764-1848 <YAI>
R:Yamuchi-Takharz, K.; Sole, M.J.; Llew, J.; Ing, D.; Llew, C.C.
Proc. Natl. Acad. Sci. U.S.A. 86, 7416-7417, 1989
A:Reference number: A94226
A:Accession: B33835
A:Molecule type: DNA
A:Residues: 1-87,'Q',89-177,1551-1732,'E',1734-1736,'T',1738-1762,'D',1764-1848 <YAI>
R:Saez, L.J.; Glanola, K.M.; McNally, E.M.; Peghali, R.; Eddy, R.; Shove, T.B.; Lelwando
Nucleic Acids Res. 15, 5443-5459, 1987
A:Title: Human cardiac myosin heavy chain genes and their linkage in the genome.
A:Reference number: A93669; MUID:87260010; PMID:3037493
A:Accession: B27858
A:Molecule type: DNA
A:Residues: 1-3,'S',5-10,'T',12,14-67 <SAB>
R:Kurabayashi, M.; Tsuchimochi, H.; Komuro, I.; Takaku, F.; Yazaki, Y.
J. Clin. Invest. 82, 524-531, 1988
A:Title: Molecular cloning and characterization of human cardiac alpha- and beta-form my
human atrium.
A:Reference number: A92770; MUID:88299163; PMID:2969919
A:Accession: A28908
A:Molecule type: mRNA
A:Residues: 1407-1532,'N',1534-1539,'W',1541-1576,'NV',1579-1704,'EO',1707-1762,'D',1766-1848 <YAI>
A:Cross-references: GB:M1664; NID:G189006; PIDN:AA6344.1; PID:G386972
A:Experimental source: fetal heart
C:Genetics:
A:Gene: GDB:MYH6
A:Cross-references: GDB:120214; OMIM:160710
A:Map position: 14q11.2-14q13
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methylace
P:178-185/Region: nucleotide-binding motif A (P-loop)
P:154-586/Region: actin binding #status predicted
P:657-679/Region: actin binding #status predicted
P:841-1339/Domain: coiled coil #status predicted <COI>
P:841-1281/Region: S2
P:1282-1939/Region: light meromyosin
P:1129/Modified site: N6,N6,N6-trimethyllysine (lys) #status predicted
P:1184/Binding site: ATP (lys) #status predicted
P:697,707/Active site: Cys #status predicted

Query Match 39.7%; Score 54; DB 1; Length 1939;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 2 RVTGPHLPKDIVSTAKAG 21
DB 665 RTTHPHFVRCILPNERKAG 684

RESULT 12
148175
myosin heavy chain alpha, cardiac muscle [similarity] - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: 148175; A23938
R:Wang, R.; Sole, M.J.; Cukerman, E.; Llew, C.C.
J. Mol. Cell. Cardiol. 26, 1155-1165, 1994
A:Title: Characterization and nucleotide sequence of the cardiac alpha-myosin heavy chain
A:Reference number: 148153; MUID:95115033; PMID:7815459
A:Accession: 148175
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-1939 <RES>
A:Cross-references: UNIPROT:P13539; GB:LL5351; NID:G402373; PIDN:AA59701.1; PID:G402374
R:Llew, C.C.; Jandreski, M.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 3175-3179, 1986
A:Title: Construction and characterization of the alpha-form of a cardiac myosin heavy c
A:Reference number: A23938; MUID:86205859; PMID:3458174

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A:Accession: A23938
A:Molecule type: mRNA
A:Residues: 1630-1843, 'R', 1845-1878, 'T', 1880-1927, 'N', 1929-1932, 1934-1939 <LIB>
A:Interons: 67/3; 115/3; 168/1; 177/2; 214/3; 245/3; 267/1; 300/1; 334/3; 381/1; 470/3; 392/2; 1453/3; 1509/1; 1550/3; 1653/3; 1721/3; 1763/3; 1855/3; 1887/3; 1932/3
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: ATP; cardiac muscle; heart; nucleotide binding; P-loop
F:188-768/Domain: myosin motor domain homology motif A (P-loop)
F:178-185/Region: nucleotide-binding motif A (P-loop)

Query Match          39.7%; Score 54; DB 2; Length 1939;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy      2  RTVHPHLPKDIVRSIAKAPG 21
      ||||| : : : |||||
      DB      665  RTVHPHFRCTIIPERRKAPG 684

RESULT 13
B87319
hypothetical protein CC0564 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: B87319
R:Name: W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo-
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249, MUID:21173698; PMID:11259647
A:Accession: B87319
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-273 <570>
A:Cross-references: UNIPROT:Q9NAN3; GB:AE005673; NID:913421758; PIDN:AAK22550.1; GSPDB:
C:Gene: CC0564

Query Match          38.2%; Score 52; DB 2; Length 273;
Best Local Similarity 40.6%; Pred. No. 7;
Matches 13; Conservative 5; Mismatches 4; Indels 10; Gaps 2;

Qy      4  THPHLP--KDIVRS-----IAKAPGKAP 25
      ||||| : ||||| : |||||
      DB      224  SRHAPRNRIIRSTLRGRDKPLCARANGRRAP 255

RESULT 14
T35963
hypothetical protein SC9C7.12 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T35963
R:Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A
submitted to the EMBL Data Library, January 1999
A:Reference number: Z21551
A:Accession: T35963
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-197 <SBB>
A:Cross-references: UNIPROT:Q9ZBJ6; EMBL:AL035161; PIDN:CAA22724.1; GSPDB:GN00070; SCOE
A:Experimental source: strain A3(2)
C:Genetic:
A:Gene: SCOEDB:SC9C7.12

Query Match          37.5%; Score 51; DB 2; Length 197;
Best Local Similarity 42.9%; Pred. No. 7;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy      3  VTHPHLPKDIVRSIAKAPGR 23
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Db 177 LAHPALAOAAVRLARIPGQR 197

RESULT 15

B46529
Ig Y heavy chain (7.88) - duck
N/Alternate names: Ig gamma chain (7.88)
C/Species: Anas platyrhynchos (domestic duck)
C/Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C/Accession: B46529; S20759
R/Magor, K.E.; Watt, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.
J. Immunol. 149, 2627-2633, 1992
A/Title: Structural relationship between the two Igy of the duck, Anas platyrhynchos: md
A/Reference number: A46529; MUID:93017865; PMID:1401901
A/Accession: B46529
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-572 <MAG>
A/Cross-references: EMBL:X65219; NID:G62442; PIDN:CAA46322.1; PID:G62443
A/Experimental source: spleen
A/Note: Sequence extracted from NCBI backbone (NCBI:P116127)
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: immunoglobulin
F;37-120/Domain: immunoglobulin homology <IMM>

Query Match 37.5%; Score 51; DB 2; Length 572;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 11; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIVRSIAKAPGK 22
Db 442 CTVOHEDLPVPLGKSIKHAAGK 463

Search completed: February 22, 2005, 07:01:47
Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 06:39:23 / Search time 175 Seconds

(without alignments)
73.154 Million cell updates/sec

Title: US-10-751-743-4
Perfect score: 136
Sequence: 1 CRYTHPLPRDVRSLAKRGRAP 25

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	77.2	429	1 EPC_RAT	P01855 ratus norv
2	86	63.2	428	1 EPC_HUMAN	P01854 homo sapien
3	80	58.8	421	1 EPC_MOUSE	P06336 mus musculu
4	59	43.4	684	2 Q90544	Q90544 ginglymose
5	55	40.4	1080	2 Q61P25	Q61P25 xenopus lae
6	54	39.7	99	2 Q9MY65	Q9MY65 ocyctolagus
7	54	39.7	1938	1 MYH6_RAT	P02563 ratus norv
8	54	39.7	1938	1 MYH6_HUMAN	P13533 homo sapien
9	54	39.7	1939	1 MYH6_MESAU	P13539 mesocricetu
10	53	39.0	538	2 Q7R2J3	Q7R2J3 neurospora
11	53	39.0	906	2 Q870P3	Q870P3 neurospora
12	52	38.2	273	2 Q9AAN3	Q9AAN3 caulobacter
13	51.5	37.9	466	2 Q6N096	Q6N096 homo sapien
14	51	37.5	197	2 Q9ZBR8	Q9ZBR8 streptomyce
15	51	37.5	1004	2 Q6P8P3	Q6P8P3 mus musculu
16	51	37.5	1935	2 Q6D1X8	Q6D1X8 xenopus tro
17	51	37.5	1938	1 MYH6_MOUSE	Q02566 mus musculu
18	51	37.5	1940	1 MYH3_HUMAN	P11055 homo sapien
19	51	37.5	1940	1 MYH3_RAT	P12847 ratus norv
20	50.5	37.1	223	2 Q8ZGJ2	Q8ZGJ2 streptomyce
21	50.5	37.1	327	1 GC4_HUMAN	P01861 homo sapien
22	50.5	37.1	330	1 GC4_MOUSE	P01865 mus musculu
23	50.5	37.1	399	1 GCAM_MOUSE	P01865 mus musculu
24	50.5	37.1	473	2 Q8TC63	Q8TC63 homo sapien
25	50.5	37.1	476	2 Q6MZX7	Q6MZX7 homo sapien
26	50.5	37.1	538	2 Q9K9R8	Q9K9R8 bacillus ha
27	50	36.8	68	2 Q9UMK8	Q9UMK8 homo sapien
28	50	36.8	736	1 MYH7_RABIT	Q04461 ocyctolagus
29	50	36.8	797	2 Q9T5U6	Q9T5U6 felis silve
30	50	36.8	1038	2 Q28699	Q28699 ocyctolagus
31	50	36.8	1510	2 Q75186	Q75186 oryza sativ

32	50	36.8	1934	1 MYH7_MESAU	P13540 mesocricetu
33	50	36.8	1935	1 MYH7_HUMAN	P12883 homo sapien
34	50	36.8	1935	1 MYH7_PIG	P79293 sus scrofa
35	50	36.8	1935	1 MYH7_RAT	P02564 ratus norv
36	50	36.8	1935	2 Q8M0U9	Q8M0U9 equus caball
37	50	36.8	1935	2 Q9BB39	Q9BB39 bos taurus
38	50	36.8	1935	2 Q9GKR1	Q9GKR1 sus scrofa
39	50	36.8	1935	2 Q91Z83	Q91Z83 mus musculu
40	49.5	36.4	336	1 GCB_MOUSE	P01866 mus musculu
41	49.5	36.4	373	2 Q76LV9	Q76LV9 mus musculu
42	49.5	36.4	374	1 SPOF_HUMAN	O43791 homo sapien
43	49.5	36.4	374	1 SPOF_MOUSE	Q6ZWS8 mus musculu
44	49.5	36.4	374	2 Q6P8B3	Q6P8B3 xenopus tro
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ALIGNMENTS

RESULT 1
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AC P01855;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig epsilon chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2).
RC STRAIN=LDU/C/MSL;
RX MEDLINE=83064537; PubMed=6292865;
RA Hellman L., Petersen U., Engstrom A., Karlsson T., Bennich H.;
RT "Structure and evolution of the heavy chain from rat immunoglobulin
E";
RL Nucleic Acids Res. 10:6041-6049(1982).
RN [2]
RP SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).
RX MEDLINE=83182019; PubMed=6820340;
RA Kindsvogel W.R., Reddy B.P., Moore J.M., Faust C.H. Jr.;
RT "A cloned cDNA probe for rat immunoglobulin epsilon heavy chain:
construction, identification, and DNA sequence.";
RL DNA 1:335-343(1982).
RN [3]
RP SEQUENCE OF 205-306 FROM N.A.
RX MEDLINE=82174576; PubMed=6803238;
RA Hellman L., Petersen U., Bennich H.;
RT "Characterization and molecular cloning of the mRNA for the heavy
epsilon chain of rat immunoglobulin E.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).
-1- SIMILARITY: Contains 4 immunoglobulin-like domains.

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CC EMBL, J00744; AAA41379.1; ALT_INIT.
DR PIR; A93442; EHRT.
DR HSSP; P01854; 1P5.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig1.4.
DR SMART; SM00407; Ig1.1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.

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KW Immunoglobulin C region; Immunoglobulin domain; Repeat.
FT NON_TER 1 89
FT DOMAIN 103 201 Ig-like 1.
FT DOMAIN 205 305 Ig-like 2.
FT DOMAIN 314 414 Ig-like 3.
FT CONFLICT 168 168 R -> N (in Ref. 2).
FT CONFLICT 308 308 P -> L (in Ref. 2).
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Best Local Similarity 79.2%; Pred. No. 7.9e-07;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CRVTHPLPDIYRSIAKAPGRKA 24
Db 289 CRVDHPFPKPIYRSITKAPGRKS 312

RESULT 2
ID EPC_HUMAN STANDARD; PRT; 428 AA.
AC P01854;
DT 21-JUL-1986 (Rel. 01. Created)
DT 21-JUL-1986 (Rel. 01. Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
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GN Name:IGH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83168897; Pubmed=6300763;
RA Kikuchi M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,
RT "Molecular cloning and nucleotide sequencing of human immunoglobulin
RL epsilon chain cDNA."
RN Nucleic Acids Res. 11;719-726(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83001945; Pubmed=6288268; DOI=10.1016/0092-8674(82)90185-4;
RA Max E.B., Batley J., Ney R., Kirsch I.R., Leder P.;
RT "Duplication and deletion in the human immunoglobulin epsilon genes."
RN Cell 29:691-699(1982).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=84236029; Pubmed=6234164;
RA Flanagan J.G., Rabbitts T.H.;
RT "The sequence of a human immunoglobulin epsilon chain constant
RL region gene, and evidence for three non-allelic genes."
RN EMBO J. 1:655-660(1982).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=84207910; Pubmed=6327276;
RA Ueda S., Nakai S., Nishida Y., Hisajima H., Honjo T.;
RT "Long terminal repeat-like elements flank a human immunoglobulin
RL epsilon pseudogene that lacks introns."
RN EMBO J. 1:1539-1544(1982).
RN [5]
RP PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND).
RA Benrich H.H., Johanson S.G.O., von Bahr-Lindstrom H.;
RL (in) Bach M.K. (eds.);
RT Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RN Marcel Dekker, New York (1978).
RN [6]
RP SEQUENCE OF 1-40; 68-114 AND 427-428 FROM N.A.
RX MEDLINE=83065234; Pubmed=6815556;
RA Kerten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Vinay J.,
RT Bell L.O., Gould H.O.;
RN "Cloning and sequence determination of the gene for the human
RL immunoglobulin epsilon chain expressed in a myeloma cell line."
RN

RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [7]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=87089848; Pubmed=3796618; DOI=10.1016/0161-5890(86)90005-2;
RA Padlan E.A., Davies D.R.;
RT "A model of the Fc of immunoglobulin E."
RN Mol. Immunol. 23:1063-1075(1986).
RN [8]
RP -1- SIMILARITY: Contains 4 Immunoglobulin-like domains.
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CC -----
CC EMBL, L00022; AAB59424.1; ALT_INIT.
CC PIR, A22771; EHHU.
CC PDB, 1F6A; X-ray; B/D=207-428.
CC PDB, 1F65; X-ray; A=207-428.
CC PDB, 1G84; NMR; A=106-210.
CC PDB, 1IGR; Model; A/B=-.
CC PDB, 1OOV; X-ray; A/B=102-428.
CC GeneW; HGNC:5522; IGH.
CC MIM, 147180; -.
CC GO; GO:0003823; P:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR03597; Ig-cl.
CC InterPro; IPR03006; Ig_MHC.
CC Pfam; PF00047; Ig; 4.
CC SMART; SM00407; IGH1; 4.
CC PROSITE; PS50835; Ig_LIKR; 4.
CC PROSITE; PS00290; Ig_MHC; 3.
KW 3D-structure; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin C region; Immunoglobulin domain; Repeat.
RN [9]
RP NON_TER 1 103
FT DOMAIN 112 210 Ig-like 1.
FT DOMAIN 214 318 Ig-like 2.
FT DOMAIN 324 423 Ig-like 3.
FT DISULFID 14 14 Ig-like 4.
FT DISULFID 15 105 Interchain (with a light chain).
FT DISULFID 29 85 Interchain (with a heavy chain).
FT DISULFID 121 121 Interchain (with a heavy chain).
FT DISULFID 135 193 Interchain (with a heavy chain).
FT DISULFID 209 299 Interchain (with a heavy chain).
FT DISULFID 239 299 Interchain (with a heavy chain).
FT CARBOHYD 345 405
FT CARBOHYD 21 21
FT CARBOHYD 49 49
FT CARBOHYD 99 99
FT CARBOHYD 146 146
FT CARBOHYD 252 252
FT CARBOHYD 275 275
FT VARIANT 359 359
FT STRAND 113 119
FT STRAND 130 138
FT STRAND 148 151
FT TURN 152 153
FT STRAND 154 156
FT STRAND 158 160
FT HELIX 163 165
FT STRAND 173 181
FT STRAND 182 186
FT HELIX 187 188
FT STRAND 191 196
FT STRAND 201 206
FT STRAND 218 221
FT HELIX 226 230
FT TURN 231 232

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CC EMBL; X01857, CAA25977.1; -.
CC EMBL; X01857, CAA25978.1; -.
CC PIR; A02144; EHMS.
CC PIR; A02145; EHMS.
CC HSSP; P01854; 1EP5.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig_c1.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 4.
CC SMART; SM00407; Igc1; 2.
CC PROSITE; PS50835; IG_LIKE; 4.
CC PROSITE; PS00290; IG_MHC; 3.
CC Glycoproteins; Immunoglobulin C region; Immunoglobulin domain.
KW NON_TER
FT 1
FT DOMAIN 1 90 CH1.
FT DOMAIN 91 197 CH2.
FT DOMAIN 198 304 CH3.
FT DOMAIN 305 421 CH4.
FT DISULFID 23 75 By similarity.
FT DISULFID 121 180 By similarity.
FT DISULFID 226 285 By similarity.
FT DISULFID 330 392 By similarity.
FT CARBOHYD 43 43 N-linked (GlcNAc...) (potential).
FT CARBOHYD 72 72 N-linked (GlcNAc...) (potential).
FT CARBOHYD 84 84 N-linked (GlcNAc...) (potential).
FT CARBOHYD 95 95 N-linked (GlcNAc...) (potential).
FT CARBOHYD 166 166 N-linked (GlcNAc...) (potential).
FT CARBOHYD 238 238 N-linked (GlcNAc...) (potential).
FT CARBOHYD 261 261 N-linked (GlcNAc...) (potential).
FT CARBOHYD 365 365 N-linked (GlcNAc...) (potential).
FT CARBOHYD 415 415 N-linked (GlcNAc...) (potential).
SQ SEQUENCE 421 AA; 47320 MW; 8F909E1F30A06B47 CRC64;

Query Match 58.8%; Score 80; DB 1; Length 421;
Best Local Similarity 62.5%; Pred. No. 0.0037;
Matches 15; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

DB 1 CRVTHPLPKDIVRSINAKPGRKA 24
285 CIVDHPDPKPIYRSITKTPGRS 308

RESULT 4
O90544 PRELIMINARY; PRT; 684 AA.
AC O90544;
DT 01-NOV-1996 (Tremblrel.01, Created)
DT 01-NOV-1996 (Tremblrel.01, Last sequence update)
DT 01-MAR-2004 (Tremblrel.26, Last annotation update)
DT Novel antigen receptor precursor.
OS Ginglymosoma citratum (Nurse shark).
OC Buthyrola; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidae; Orectolobiformes;
OC Ginglymosomatidae; Ginglymosoma.
OX NCBI_TaxID=7801;
RA [1]
RA SEQUENCE FROM N.A.
RC TISSUE-Spleen;
RX MERRILL-95181140; PubMed=7877689; DOI=10.1038/374169a0;
RA Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C.,
RA Flajnik M.F.;
RT "A new antigen receptor gene family that undergoes rearrangement and
RT extensive somatic diversification in sharks.";
RL Nature 374:168-173(1995).
DR EMBL; U18701; AAB48195.1; -.
DR PIR; S60266; S60266.
DR HSSP; P01842; IAOK.
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DR GO:0004872; F:receptor activity; IEA.
 DR Pfam; PF07654; Cl-sec; 3.
 DR SMART; SM0047; Ig; 2.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 DR Receptor; Signal.
 FT SIGNAL 1 18 Potential
 CHAIN 19 684 novel antigen receptor.
 SQ SEQUENCE 684 AA; 75224 MW; 2F9D2071CDAD56FD CRC64;

Query Match 43.4%; Score 59; DB 2; Length 684;
 Best Local Similarity 50.0%; Pred. No. 7.4;
 Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 Db 645 CLVGHPSLRDLIRSRNSNGK 666

RESULT 5
 ID Q6IP25 PRELIMINARY; PRT; 1080 AA.
 AC Q6IP25;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE LOC32141 protein (Fragment).
 GN Name=LOC32141;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=22388257; PubMed=2477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Colling P.B., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Ditzchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
 RA Brownstein M.J., Udell T.B., Toshyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Richards S., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 RA Pabey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
 RA Krzywinski M.I., Skalka U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.,
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 initiative.";
 RT Dev. Dyn. 225:384-391 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA Klein S., Strausberg R.,
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR BMBL; BC072094; AAH72094.1; -.

DR HSPB; P24733; 1KK8.
 DR GO:00016459; C:myosin; IEA.
 DR GO:0005524; F:ATP binding; IEA.
 DR GO:0003774; F:motor activity; IEA.
 DR InterPro; IPRO00048; IQ region.
 DR InterPro; IPRO01609; Myosin head.
 DR InterPro; IPRO04009; Myosin_N.
 DR Pfam; PF00612; IQ; 2.
 DR Pfam; PF00063; Myosin_head; 1.
 DR Pfam; PF02736; Myosin_N; 1.
 DR PRINTS; PR00193; MYOSINHEAVY.
 DR ProDom; PD000355; MYOSINHEAVY.
 DR SMART; SM00015; IQ; 2.
 DR SMART; SM00242; MYSC; 1.
 DR PROSITE; PS50096; IQ; 1.
 FT NON_TER 1080 1080
 SQ SEQUENCE 1080 AA; 123936 MW; 5BDC6234B598B9F5 CRC64;

Query Match 40.4%; Score 55; DB 2; Length 1080;
 Best Local Similarity 47.6%; Pred. No. 46;
 Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 Db 660 RTTHPFPVRCILPNERKAPG 680

RESULT 6
 ID Q9WYS5 PRELIMINARY; PRT; 99 AA.
 AC Q9WYS5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin heavy chain (Fragment).
 GN Name=myh6;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand White; TISSUE=Heart;
 RA Sayed R.A., Grace A.A., Vandenberg J.I.,
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ291317; CAB94849.1; -.
 DR HSPB; P13538; 2MTS.
 DR GO:00016459; C:myosin; IEA.
 DR GO:0005524; F:ATP binding; IEA.
 DR GO:0003774; F:motor activity; IEA.
 DR InterPro; IPRO01609; Myosin head.
 DR Pfam; PF00063; Myosin_head; 1.
 FT NON_TER 99 99
 SQ SEQUENCE 99 AA; 10933 MW; 3961CA1047DB2B0C CRC64;

Query Match 39.7%; Score 54; DB 2; Length 99;
 Best Local Similarity 50.0%; Pred. No. 5.5;
 Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 Db 79 RTTHPFPVRCILPNERKAPG 98

RESULT 7
 ID MYH6_RAT
 AC P02563; Q63351; STANDARD; PRT; 1938 AA.
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Myosin heavy chain, cardiac muscle alpha isoform (MyHC-alpha).

GN Name=Myh6;
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=90016822; PubMed=2798111;
 RA Kraft R., Bravo-Zehnder M., Taylor D., Lelwand L.A.;
 RT "Complete nucleotide sequence of full length cDNA for rat alpha
 RT cardiac myosin heavy chain.";
 RL Nucleic Acids Res. 17:7527-7528(1989).
 RN [2]
 RP DISCUSSION OF SEQUENCE.
 RX MEDLINE=9013319; PubMed=2614840;
 RA McNally E.M., Kraft R., Bravo-Zehnder M., Taylor D., Lelwand L.A.;
 RT "Full-length rat alpha and beta cardiac myosin heavy chain sequences.
 RT Comparisons suggest a molecular basis for functional differences.";
 RL J. Mol. Biol. 220:665-671(1989).
 RN [3]
 RP SEQUENCE OF 1-167 FROM N.A.
 RX MEDLINE=84194059; PubMed=5585819;
 RA Mahdavi V., Chambers A.P., Nadal-Ginard B.;
 RT "Cardiac alpha- and beta-myosin heavy chain genes are organized in
 RT tandem.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:2626-2630(1984).
 RN [4]
 RP SEQUENCE OF 1512-1938 FROM N.A.
 RX MEDLINE=8220036; PubMed=7045682;
 RA Mahdavi V., Periasamy M., Nadal-Ginard B.;
 RT "Molecular characterization of two myosin heavy chain genes expressed
 RT in the adult heart.";
 RL Nature 297:659-664(1982).
 RN [5]
 RP SEQUENCE OF 1872-1938 FROM N.A.
 RC STRAIN=Mistral; TISSUE=Heart;
 RX MEDLINE=85179510; PubMed=6241892;
 RA Mahdavi V., Lompre A.M., Chambers A.P., Nadal-Ginard B.;
 RT "Cardiac myosin heavy chain isozytic transitions during development
 RT and under pathological conditions are regulated at the level of mRNA
 RT availability.";
 RL Eur. Heart J. 5:181-191(1984).
 CC -1- FUNCTION: Muscle contraction.
 CC -1- SUBUNIT: Myosin is a hexameric protein that consists of 2
 CC heavy chain subunits (MHC), 2 alkali light chain subunits (MLC)
 CC and 2 regulatory light chain subunits (MLC-2).
 CC -1- DOMAIN: The rodlike tail sequence is highly repetitive, showing
 CC cycles of a 28-residue repeat pattern composed of 4 heptapeptides,
 CC characteristic for alpha-helical coiled coils.
 CC -1- MISCELLANEOUS: Each myosin heavy chain can be split into 1 light
 CC meromyosin (MM) and 1 heavy meromyosin (HMM). It can later be
 CC split further into 2 globular subfragments (S1) and 1 rod-shaped
 CC subfragment (S2).
 CC -1- MISCELLANEOUS: The cardiac alpha isoform is a 'fast' ATPase
 CC myosin, while the beta isoform is a 'slow' ATPase.
 CC -1- SIMILARITY: Contains 1 myosin-like globular head domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL: X15938; CAA34064.1; -;
 DR EMBL: K01464; AAA41648.1; -;
 DR EMBL: J00751; AAA41653.1; -;
 DR EMBL: M32697; AAA41658.1; -;
 DR PIR: S06005; S06005.

DR HSSP; P24733; IKOM.
 DR RGD; 62029; Myh6.
 DR InterPro; IPR000048; IQ_region.
 DR InterPro; IPR001609; Myosin_head.
 DR InterPro; IPR004009; Myosin_N.
 DR InterPro; IPR002928; Myosin_tail.
 DR Pfam; PF00642; IQ_2.
 DR Pfam; PF00653; Myosin_head_1.
 DR Pfam; PF02736; Myosin_N_1.
 DR Pfam; PF01576; Myosin_tail_1.
 DR PRINTS; PR00193; MYOSINHEAVY.
 DR ProDom; PD000355; Myosin_head_1.
 DR PROSITE; PS00096; IQ_1.
 KW Actin-binding; ATP-binding; Calmodulin-binding; Coiled coil;
 KW Methylation; Multigene family; Muscle protein; Myosin; Thick filament.
 FT DOMAIN 1 781
 FT DOMAIN 782 811
 FT DOMAIN 842 1938
 FT NP BIND 177 184
 FT DOMAIN 656 678
 FT DOMAIN 758 772
 FT DOMAIN 789 806
 FT DOMAIN 815 832
 FT MOD RES 128 128
 FT CONFLICT 13 13
 FT CONFLICT 46 46
 FT CONFLICT 51 52
 FT CONFLICT 87 87
 FT CONFLICT 109 109
 FT CONFLICT 1566 1566
 FT CONFLICT 1575 1575
 FT CONFLICT 1721 1721
 FT CONFLICT 1852 1852
 FT CONFLICT 1870 1870
 FT CONFLICT 1934 1934
 SQ SEQUENCE 1938 AA; 223507 MW; D7BD33FC2B19E3C2 CRC64;
 Query Match 39 %; Score 54; DB 1; Length 1938;
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;
 Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 Db 664 RTHPHFVACITPERKAPG 683
 Qy 2 RVTHPHLPDIVSIKAPG 21
 ID MYH6 HUMAN STANDARD; PRT; 1939 AA.
 AC P13533; Q13943; Q14906; Q14907;
 DT 01-JUN-1990 (Rel. 13, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Myosin heavy chain, cardiac muscle alpha isoform (MYHC-alpha).
 GN Name=Myh6; Synonyms=MYHCA;
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92133665; PubMed=1776652;
 RA Matsuo K., Beisel K.W., Furutani M., Arai S., Takao A.;
 RT "Complete sequence of human cardiac alpha-myosin heavy chain gene and
 RT amino acid comparison to other myosins based on structural and
 RT functional differences.";
 RL Am. J. Med. Genet. 41:537-547(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94140346; PubMed=8307559;
 RA Bep T.A., Dixon I.M., Wang H.Y., Sole M.J., Llew C.-C.;
 RT "Structural organization of the human cardiac alpha-myosin heavy chain
 RT gene (MYH6).";

[illegible]

```

CC -1- SUBUNIT: Muscle myosin is a hexameric protein that consists of 2
CC heavy chain subunits (MHC), 2 alkali light chain subunits (MLC)
CC and 2 regulatory light chain subunits (MLC-2).
CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
CC -1- DOMAIN: The rodlike tail sequence is highly repetitive, showing
CC cycles of a 28-residue repeat pattern composed of 4 heptapeptides,
CC characteristic for alpha-helical coiled coils.
CC -1- MISCELLANEOUS: Each myosin heavy chain can be split into 1 light
CC meromyosin (LM) and 1 heavy meromyosin (HMM). It can later be
CC split further into 2 globular subfragments (S1) and 1 rod-shaped
CC subfragment (S2).
CC -1- MISCELLANEOUS: The cardiac alpha isoform is a 'fast' ATPase
CC myosin, while the beta isoform is a 'slow' ATPase.
CC -1- SIMILARITY: Contains 1 IQ domain.
CC -1- SIMILARITY: Contains 1 myosin-like globular head domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: I15351; AAB59701.1; -
DR EMBL: M12995; AAA37081.1; -
DR F1: 148175; 148175.
DR HSSP: P24733; 1KQM.
DR InterPro: IPR0000048; IQ region.
DR InterPro: IPR001609; Myosin head.
DR InterPro: IPR004009; Myosin N.
DR InterPro: IPR002928; Myosin_tail.
DR Pfam: PF00612; IQ; 2.
DR Pfam: PF00063; Myosin_head; 1.
DR Pfam: PF02736; Myosin_N; 1.
DR Pfam: PF01576; Myosin_tail_1; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR PRODOM: PD000355; Myosin_head; 1.
DR PROSITE: PS50096; IQ; 1.
KW Actin-binding; ATP-binding; Calmodulin-binding; Coiled coil;
KW Myofibrillogenesis; Multigene family; Muscle protein; Myosin; Thick filament.
KW Myosin head-1like.
FT DOMAIN 1 782 812
FT DOMAIN 842 1939
FT DOMAIN 1439 1443
FT NP BIND 178 185
FT DOMAIN 657 679
FT DOMAIN 759 773
FT MOD RES 129 129
FT CONFLICT 1633 1633
FT CONFLICT 1651 1651
FT CONFLICT 1686 1687
FT CONFLICT 1693 1693
FT CONFLICT 1844 1844
FT CONFLICT 1879 1879
FT CONFLICT 1885 1885
FT CONFLICT 1907 1907
FT CONFLICT 1928 1928
FT CONFLICT 1933 1935
SQ SEQUENCE 1939 AA; 223626 MW; DBC8297DFE83115A CRC64;

Query Match 39.7%; Score 54; DB 1; Length 1939;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

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Qy 2 RVTGPHLPKDIIVRSIAKAPG 21
 Db 665 RTTHPHFVRCIIIPERKAPG 684

RESULT 10
 Q7RZJ3 PRELIMINARY; PRT; 538 AA.

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AC Q7RZJ3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NC004012.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxId=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR743;
RA Galagan J.E., Calvo S.B., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell L., Rehm B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Saiteremikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Greer S.,
RA Kamal M., Kamysheva M., Mauceli E., Bielke C., Rudd S., Friedman D.,
RA Krysotova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Omani S.A.,
RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Varden O., Plamann M., Seltzer S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebdole D.J., Frettag M.,
RA Paulsen I., Sachs M.S., Lander B.S., Nussbaum C., Birren B.,
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."
RL Nature 0:0-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABX01000718; EAA28391.1; -
DR EMBL: AABX01000718; EAA28391.1; -
SQ SEQUENCE 538 AA; 61419 MW; 6C98D237618799B4 CRC64;

Query Match 39.0%; Score 53; DB 2; Length 538;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 11; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

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Qy 1 CRVTGPHLPKDIIVRSIAKAPG 22
 Db 122 CRATFPGMKKIDDTAKGPFK 143

RESULT 11
 Q870P3 PRELIMINARY; PRT; 906 AA.
 ID Q870P3;
 AC Q870P3;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein 49D12.100.
 GN Name=49D12.100;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxId=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Algen V., Hobeisel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RP [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BX295540; CAD79685.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 906 AA; 102137 MW; 71ED849AF8B03146 CRC64;

Query Match 39.0%; Score 53; DB 2; Length 906;
 Best Local Similarity 50.0%; Pred. No. 76;
 Matches 11; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 CRYTHRLPKDIVRS-TAKAPGK 22
DB 122 CRAFTPGMLKEIDDTYAKGPFK 143

RESULT 12

Q9AAN3 PRELIMINARY; PRT; 273 AA.

AC Q9AAN3; 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein CC0564.
GN OrderedLocustNames=CC0564.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxId=155892;
RN [1]

SEQUENCE FROM N.A.

RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298,
RA Nieman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Porocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
RA Berry K.J., Uteback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.,
RT "Complete genome sequence of Caulobacter crescentus."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE05730; AAK2550.1; -.
DR PIR; B87319; B87319.
SQ SEQUENCE 273 AA; 29461 MW; C1C6D2FB7E432082 CRC64;

Query Match

Best Local Similarity 38.2%; Score 52; DB 2; Length 273;
Matches 13; Conservative 5; Mismatches 4; Indels 10; Gaps 2;

QY 4 THPHLP-KDIVRS-----TAKAPGRAP 25
DB 224 SRPHAPNRDIIRSTLCGRDPLCARANGRRAP 255

RESULT 13

Q6N096 PRELIMINARY; PRT; 466 AA.

AC Q6N096; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686115196.
GN Name=DKFZp686115196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]

SEQUENCE FROM N.A.

RC TISSUE=Human esophagus tumor;
RG The German Human CDNA Consortium;
RG Wamutt R., Heubner D., Mewes H.W., Weil B., Oesanger A.,
RA Fobo G., Han M., Wiemann S., EMBL/genbank/DBJ databases.
RL Submitted (Aug-2003) to the EMBL/genbank/DBJ databases.
DR EMBL; BX640620; CAE45774.1; -.
DR HSSP; F01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_c1.

DR InterPro; IPR00306; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG1; 2.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 466 AA; 50926 MW; 01B91B74BD6D57C4 CRC64;

Query Match 37.9%; Score 51.5; DB 2; Length 466;
Best Local Similarity 46.2%; Pred. No. 63;
Matches 12; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 CRYTHRLPKDIVRS-TAKAPGK-RAP 25
DB 340 CRYSNKALPAPLEKTIISAKGQPREP 365

RESULT 14

Q9ZBJ8 PRELIMINARY; PRT; 197 AA.

AC Q9ZBJ8; 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein SC06476.
GN ORFNames=SC9C7.12;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxId=1902;
RN [1]

SEQUENCE FROM N.A.

RC STRAIN=A3(2) / M45;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-W., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieffer H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornby T., Howarth S.,
RA Huang C.-H., Kieffer T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajadream M.A., Rutherford K.M., Ruter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrall B.G., Parkhill J.,
RA Hopwood D.A.,
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2)."
RL Nature 417:141-147(2002).
DR EMBL; AL939127; CNA22724.1; -.
DR PIR; T35963; T35963.
DR InterPro; IPR008938; ARM.
DR InterPro; IPR004155; PBS_lyase_HEAT.
DR Pfam; PF03130; HEAT_PBS; 1.
DR SMART; SM00567; EZ_HEAT; 4.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 197 AA; 21061 MW; 6AB3643C5570AC1 CRC64;

Query Match 37.5%; Score 51; DB 2; Length 197;
Best Local Similarity 42.9%; Pred. No. 31;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 3 VTHPHLP-KDIVRS-TAKAPGR 23
DB 177 LAMPALAAVAAALAIRPQR 197

RESULT 15

Q6PBP3 PRELIMINARY; PRT; 1004 AA.

AC Q6PBP3; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE Myh6 protein (Fragment).
GN Name=Myh6
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090,
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung and heart;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helen F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedl T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.B., Scherch A., Schein J.E.,
RA Jones S.V., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung and heart;
RA Straubeberg R.L.
RL Submitted (NCV-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC061145; AAH61145.1; -
DR HSBP; P24733; IKK8.
DR GO; GO:0007522; P:Visceral muscle development; IMP.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR001609; Myosin_head.
DR InterPro; IPR004009; Myosin_N.
DR Pfam; PF00612; IQ; 2.
DR Pfam; PF00063; Myosin_head; 1.
DR Pfam; PF02736; Myosin_N; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR ProDom; PD000355; Myosin_head; 1.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PSS0096; IQ; 1.
FT NOX TER 1004 1004
SQ SEQUENCE 1004 AA, 115137 MW, 0D8457AF2451F6EB CRC64,

OY 2 RVTHPHLPKDIIVRSIAKAPG 21
: ||||| : : |||||
Db 665 KTHPHFVRCIIIPNERRKAPG 684

Query March 37.5%; Score 51; DB 2; Length 1004;
Best Local Similarity 45.0%; Pred. NO. 1.7e+02;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Search completed: February 22, 2005, 07:00:16
Job time : 177 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 07:11:31, Search time 38 Seconds
(without alignments)
63.301 Million cell updates/sec

Title: US-10-751-743-4

Perfect score: 136
Sequence: 1 CRTHPHLPKDIYRSIAKAPGRAP 25

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4989

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 79:*

1: P1r1:*

2: P1r2:*

3: P1r3:*

4: P1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	21.3	25	2 S07770	histone H2B.1, spe
2	28	20.6	11	2 S78765	ribosomal protein
3	27	19.9	16	2 P11351	Ig heavy chain DJ
4	27	19.9	20	2 A41439	acid ribonuclease
5	27	19.9	25	1 Z1BPG4	gene J protein - p
6	26.5	19.5	20	2 A36016	granulocyte inhibi
7	26.5	19.5	22	2 P00143	polygalacturonase
8	26	19.1	13	2 S32551	glutathione transf
9	26	19.1	15	4 J38336	hypothetical TBL/M
10	26	19.1	20	2 JPO055	ribosomal protein
11	26	19.1	22	2 H30608	Ig kappa chain V-I
12	26	19.1	22	2 D30609	Ig kappa chain V-I
13	26	19.1	24	2 B30609	Ig kappa chain V-I
14	26	19.1	24	2 JPO052	ribosomal protein
15	25	18.4	10	2 H37196	bradykinin-potent
16	25	18.4	15	2 PA0071	superoxide dismuta
17	25	18.4	15	2 I50503	agrin - electric r
18	25	18.4	17	2 D22595	bombolitin IV - Am
19	25	18.4	20	2 F80028	flagellar motor sw
20	25	18.4	20	2 H28949	ribosomal protein
21	25	18.4	21	2 B33600	glutamate-ammoma
22	25	18.4	22	2 D47256	kinetoplast DNA-as
23	25	18.4	24	2 G85602	hypothetical prote
24	25	18.4	25	2 A60621	homocytropin - Act
25	25	18.4	10	2 B37196	bradykinin-potent
26	24	17.6	20	2 S23981	outer layer protei
27	24	17.6	20	2 S46479	retinoid-X-recepto
28	24	17.6	21	2 S51066	ribosomal protein
29	24	17.6	22	2 C42856	hypothetical prote

30	24	17.6	22	2 S42567	cytochrome-b5 redu
31	23.5	17.3	23	2 PS0273	hypothetical prote
32	23.5	17.3	23	2 A41263	kinase-related tra
33	23	16.9	10	2 S77990	cytochrome-c oxida
34	23	16.9	15	2 B39109	hypothetical 1.5K
35	23	16.9	16	2 PH1317	Ig heavy chain DJ
36	23	16.9	16	2 S65709	major allergen Myr
37	23	16.9	18	2 B27504	histone H2B - mous
38	23	16.9	19	2 PA0012	superoxide dismuta
39	23	16.9	20	2 S09025	carboxylesterase (
40	23	16.9	20	2 A42865	Ca2+/calmodulin-de
41	23	16.9	21	2 S57568	T cell receptor V-
42	23	16.9	22	2 C48186	ATPase R1 subunit
43	23	16.9	23	2 S23518	stromelysin (EC 3.
44	23	16.9	23	2 S72535	probable acr-2 reg
45	22	16.2	7	2 A44428	platelet aggregati

ALIGNMENTS

RESULT 1
S07770 histone H2B.1, sperm - sea urchin (Schinus esculentus) (fragment)
C:Species: Schinus esculentus
C>Date: 30-Sep-1991 #sequence_rev: 30-Sep-1991 #ext_change 09-Jul-2004
R: Hill, C.S./ Thomas, J.O.
Eur. J. Biochem. 187, 145-153, 1990
A: Title: Core histone-DNA interactions in sea urchin sperm chromatin. The N-terminal ta
A: Reference number: S07769; PMID:90126812; PMID:2298202
A: Accession: S07770
A: Molecule type: protein
A: Residues: 1-25 <HIL>
A: Cross-references: UNIPROT: P13281
C: Keywords: chromosomal protein; DNA binding; nucleosome core; nucleus

Query Match 21.3%; Score 29; DB 2; Length 25;
Best Local Similarity 62.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 4 KSPTKRSF 11

RESULT 2
S8765 ribosomal protein MRP-524, mitochondrial - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Sep-1999 #sequence_rev: 20-Sep-1999 #ext_change 09-Jul-2004
C: Accession: S78765
R: Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A: Reference number: S78760
A: Accession: S78765
A: Molecule type: protein
A: Residues: 1-11 <GRA>
A: Cross-references: UNIPROT: Q7M374
C: Keywords: mitochondrial
F: 1-11/Product: ribosomal protein MRP-524 (fragment) #status experimental <MAT>

Query Match 20.6%; Score 28; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

DB 5 HHPLPKDIYR 14
2 HVDVPRDLTK 11

RESULT 3

PH1351
 Ig heavy chain DJ region (clone C100-109B) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #ext_change 07-May-1999
 C/Accession: PH1351
 R/Wasserman, R.; Gallil, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A/Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
 A/Reference number: PH1302; MUID:93094761; PMID:1460419
 A/Accession: PH1351
 A/Molecule type: DNA
 A/Residues: 1-16 <NMS>
 C/Keywords: heterotetramer; immunoglobulin

Query Match 19.9%; Score 27; DB 2; Length 16;
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 16 IKAPGKAP 25
 | | | | |
 Db 7 ISTRPGARP 16

RESULT 4
 A1439
 acid ribonuclease (EC 3.1.-.-) - bovine (fragment)
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #ext_change 09-Jul-2004
 C/Accession: A1439
 R/Ohg1, K.; Sanda, A.; Takizawa, Y.; Irie, M.
 J. Biochem. 103, 267-273, 1988
 A/Title: Purification of acid ribonucleases from bovine spleen.
 A/Reference number: A1439; MUID:88227899; PMID:3131316
 A/Accession: A1439
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-20 <OHG>
 A/Cross-references: UNIPROT:Q7M2NS
 C/Keywords: hydrolase

Query Match 19.9%; Score 27; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 2e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 5 HPHLPKDI 12
 | : | | |
 Db 9 HLYFPKDL 16

RESULT 5
 ZJBRG4
 gene J protein - phage G4
 C/Species: phage G4
 C/Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #ext_change 09-Jul-2004
 C/Accession: A04259
 R/Godson, G.N.; Barrell, B.G.; Staden, R.; Fiddes, J.C.
 Nature 276, 236-247, 1978
 A/Title: Nucleotide sequence of bacteriophage G4 DNA.
 A/Reference number: A93200; MUID:79053264; PMID:714153
 A/Accession: A04259
 A/Molecule type: DNA
 A/Residues: 1-25 <GOD>
 A/Cross-references: UNIPROT:P03652; GB:J02454; GB:M10724; GB:M11404; GB:V00657; NID:g156
 C/Comment: Gene J protein is one of the structural components of the bacteriophage coat.
 C/Superfamily: phage phi-X174 gene J protein
 C/Keywords: DNA binding

Query Match 19.9%; Score 27; DB 1; Length 25;
 Best Local Similarity 43.8%; Pred. No. 2.5e+03;
 Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 QY 8 LKQIVRSIAKPKR 23
 : | | | | | | |

Db 1 MKKSIRSGKSKAR 16

RESULT 6
 A36016
 granulocyte inhibitory protein - human
 C/Species: Homo sapiens (man)
 C/Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #ext_change 09-Jul-2004
 C/Accession: A36016
 R/Hoerl, W.H.; Haag-Weber, M.; Georgopoulos, A.; Block, L.H.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6353-6357, 1990
 A/Title: Physicochemical characterization of a polypeptide present in uremic serum that
 A/Reference number: A36016; MUID:90349614; PMID:2385596
 A/Accession: A36016
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-20 <HOR>
 A/Cross-references: UNIPROT:Q7M4S4
 C/Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 19.5%; Score 26.5; DB 2; Length 20;
 Best Local Similarity 36.8%; Pred. No. 2.4e+03;
 Matches 7; Conservative 5; Mismatches 2; Indels 5; Gaps 1;
 QY 11 DIVR-----STAKPKRA 24
 | | | | | : : : : :
 Db 1 DIVMTQSPPTLVSPPERA 19

RESULT 7
 PQ0143
 polygalacturonase (EC 3.2.1.15) p26 - evening primrose (fragment)
 C/Species: Oenothera organensis (evening primrose)
 C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #ext_change 09-Jul-2004
 C/Accession: PQ0143
 R/Brown, S.M.; Crouch, M.L.
 Plant Cell 2, 263-274, 1990
 A/Title: Characterization of a gene family abundantly expressed in Oenothera organensis
 A/Reference number: Q00992; MUID:93005658; PMID:2152116
 A/Accession: PQ0143
 A/Molecule type: mRNA
 A/Residues: 1-22 <BRO>
 A/Cross-references: UNIPROT:Q969B8
 A/Experimental source: pollen
 C/Comment: This protein is specifically translated in the pollens.
 C/Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 19.5%; Score 26.5; DB 2; Length 22;
 Best Local Similarity 38.1%; Pred. No. 2.6e+03;
 Matches 8; Conservative 3; Mismatches 9; Indels 1; Gaps 1;
 QY 1 CRVTHPLPDYRSIAKAPG 21
 | : | : | : | : | : |
 Db 1 CTTTNAQL-FDITKYGAKDGG 20

RESULT 8
 S32551
 glutathione transferase (EC 2.5.1.18) mu (isoform pi 6.4) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #ext_change 09-Jul-2004
 C/Accession: S32551; S32550
 R/Singhal, S.S.; Saxena, M.; Ahmad, H.; Anaschi, Y.C.
 Biochim. Biophys. Acta 1116, 137-146, 1992
 A/Title: Glutathione S-transferases of mouse liver: sex-related differences in the expe
 A/Reference number: S32546; MUID:92256466; PMID:1581342
 A/Accession: S32551
 A/Molecule type: protein
 A/Residues: 1-13 <SINI>
 A/Cross-references: UNIPROT:Q7M059
 A/Experimental source: female

A/Accession: S32550
 A/Molecule type: protein
 A/Residues: 1-13 <SIN2>
 A/Experimental source: male
 C/Keywords: transferase

Query Match 19.1%; Score 26; DB 2; Length 13;
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RATHP 6
 DB 9 RLTHP 13

RESULT 9

I38336
 hypothetical TEL/MN1 mutant fusion protein type I - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 21-Feb-1997 #sequence_rev1510n 21-Feb-1997 #text_change 20-Apr-2000
 C/Accession: I38336
 R/Buil's, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A.G.
 Oncogene 10, 1511-1519, 1995
 A/Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in fusion
 A/Reference number: 138031; PMID:95249265; PMID:7731705
 A/Accession: I38336
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-15 <BUI>
 A/Cross-references: EMBL:X85026; NID:9971473; PID:CA59399.1; PID:9971474
 C/Comment: This sequence is the chimeric product of a translocation mutation.
 C/Genetic:
 A/Gene: ETV6/MN1, TEL/MN1
 A/Map position: 22q11/12p13
 C/Keywords: fusion protein

Query Match 19.1%; Score 26; DB 4; Length 15;
 Best Local Similarity 66.7%; Pred. No. 2.1e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 HLPKDI 12
 DB 6 HLPKDI 11

RESULT 10

JP0055
 ribosomal protein L30 - Bacillus polymyxa (fragment)
 C/Species: Bacillus polymyxa
 C/Date: 10-Mar-1994 #sequence_rev1510n 28-Oct-1994 #text_change 09-Jul-2004
 C/Accession: JP0055
 R/Ochi, K.
 submitted to JIPID, February 1994
 A/Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal pr
 A/Reference number: JP0042

A/Accession: JP0055
 A/Molecule type: protein
 A/Residues: 1-20 <OCH>
 A/Cross-references: UNIPROT:Q7M163
 C/Superfamily: Escherichia coli ribosomal protein L30
 C/Keywords: protein biosynthesis; ribosome

Query Match 19.1%; Score 26; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 2.8e+03;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 12 IYRSIAKAPG 21
 DB 7 LVRSLSIRPG 16

RESULT 11

H30608

Ig kappa chain V-II region (Ste) - human (fragment)

C/Species: Homo sapiens (man)
 C/Date: 29-Jun-1989 #sequence_rev1510n 29-Jun-1989 #text_change 09-Jul-2004
 C/Accession: H30608
 R/Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjona, M.L.; Fernandez, J.; Carson, D.; Sol
 J. Immunol. 142, 3158-3163, 1989
 A/Title: Structural and idiotypic characterization of the L chains of human IGM autoant
 A/Reference number: A30601; PMID:89215279; PMID:2496160
 A/Accession: H30608
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-22 <GON>
 A/Cross-references: UNIPROT:Q9UL78
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin

Query Match 19.1%; Score 26; DB 2; Length 22;
 Best Local Similarity 40.0%; Pred. No. 3e+03;
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 15 SIAKAPKRA 24
 DB 10 TLSVSRGERRA 19

RESULT 12

D30609
 Ig kappa chain V-III regions (Jon and Mit) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 29-Jun-1989 #sequence_rev1510n 29-Jun-1989 #text_change 09-Jul-2004
 C/Accession: D30609
 R/Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjona, M.L.; Fernandez, J.; Carson, D.; Sol
 J. Immunol. 142, 3158-3163, 1989
 A/Title: Structural and idiotypic characterization of the L chains of human IGM autoant
 A/Reference number: A30601; PMID:89215279; PMID:2496160
 A/Accession: D30609
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-22 <GON>
 A/Cross-references: UNIPROT:Q9UL85
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin

Query Match 19.1%; Score 26; DB 2; Length 22;
 Best Local Similarity 40.0%; Pred. No. 3e+03;
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 15 SIAKAPKRA 24
 DB 10 TLSVSRGERRA 19

RESULT 13

B30609
 Ig kappa chain V-III region (She) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 29-Jun-1989 #sequence_rev1510n 29-Jun-1989 #text_change 09-Jul-2004
 C/Accession: B30609
 R/Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjona, M.L.; Fernandez, J.; Carson, D.; Sol
 J. Immunol. 142, 3158-3163, 1989
 A/Title: Structural and idiotypic characterization of the L chains of human IGM autoant
 A/Reference number: A30601; PMID:89215279; PMID:2496160
 A/Accession: B30609
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-24 <GON>
 A/Cross-references: UNIPROT:Q9UL83
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin

Query Match 19.1%; Score 26; DB 2; Length 24;
 Best Local Similarity 40.0%; Pred. No. 3.3e+03;
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 15 SIKAPKRA 24
 ::: : ||: ||
 Db 10 TLVSFGERA 19

RESULT 14

JP0052
 ribosomal protein l30 - *Bacillus macquariensis* (fragment)
 C:Species: *Bacillus macquariensis*
 C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
 C:Accession: JP0052
 R:Ochi, K.
 submitted to JIPID, February 1994
 A:Description: Phylogenetic diversity in the genus *Bacillus* and comparative ribosomal pr
 A:Reference number: JP0042
 A:Accession: JP0052
 A:Molecule type: protein
 A:Residues: 1-24 <OCH>
 A:Cross-references: UNIPROT:Q7M162
 C:Superfamily: *Bacterichia coli* ribosomal protein l30
 C:Keywords: protein biosynthesis; ribosome

Query Match 19.1%; Score 26; DB 2; Length 24;
 Best Local Similarity 50.0%; Pred. No. 3.3e+03;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 12 IVRSIAKPG 21
 : ||: ||
 Db 8 LVRSILGRPG 17

RESULT 15

H37196
 bradykinin-potentiating peptide 8 - *Island jararaca*
 C:Species: *Bothrops insularis* (Island jararaca)
 C:Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
 C:Accession: H37196
 R:Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
 J. Protein Chem. 9, 221-227, 1990
 A:Title: Primary structure and biological activity of bradykinin potentiating peptides f
 A:Reference number: A37196; WUID:90351557; PMID:2386615
 A:Accession: H37196
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <CIN>
 A:Cross-references: UNIPROT:P30426
 C:Keywords: pyroglutamic acid
 F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.4%; Score 25; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 HPNIP 9
 ||: ||
 Db 5 HPNIP 9

Search completed: February 22, 2005, 07:20:44
 UDB time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 07:01:55, Search time 175 Seconds

(without alignments)
73.154 Million cell updates/sec

Title: US-10-751-743-4

Perfect score: 136
Sequence: 1 CRVTHPLPKDVRISAKAPGKAP 25

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 16988

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Uniprot 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	25.7	19	1	CKAD CONGE
2	33	24.3	23	1	Q6TMS4
3	31	22.8	18	1	CTIC_LITCI
4	30	22.1	18	2	Q9BQ70
5	30	22.1	19	2	Q9ORH8
6	30	22.1	20	2	Q99JV2
7	29	21.3	16	2	Q9T2R0
8	29	21.3	18	1	CTIA_LITCI
9	29	21.3	19	2	Q16271
10	29	21.3	21	2	Q6A1F4
11	29	21.3	25	1	H2B1 ECHHS
12	28	20.6	11	2	Q7M374
13	28	20.6	22	2	Q9MK47
14	28	20.6	24	2	Q9L7N8
15	27	19.9	12	1	PEK4_PBRAM
16	27	19.9	15	2	Q9UEM3
17	27	19.9	20	2	Q9UMI8
18	27	19.9	20	2	Q7M2N5
19	27	19.9	21	2	Q9N0Y5
20	27	19.9	22	2	Q6UDH2
21	27	19.9	24	2	Q7XAX3
22	27	19.9	25	1	VGJ_BPG4
23	27	19.9	25	2	Q7RI27
24	27	19.9	25	2	Q6QF50
25	26.5	19.5	17	2	Q9TRW3
26	26.5	19.5	19	1	TRP3_LBUMA
27	26.5	19.5	20	2	Q7M454
28	26.5	19.5	22	2	Q9S9B8
29	26	19.1	12	2	Q7KYL7
30	26	19.1	13	1	UP71_LITWM
31	26	19.1	13	2	Q7M059

ALIGNMENTS

RESULT 1	CKAD CONGE	STANDARD	PRT	19 AA
ID	CKAD CONGE	STANDARD	PRT	19 AA
AD	P60274			
DT	29-MAR-2004 (Rel. 43, Created)			
DT	29-MAR-2004 (Rel. 43, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Alpha-conotoxin GID.			
OS	Conus geographus (Geography cone).			
OC	Bakaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;			
OC	Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;			
OC	Neogastropoda; Conidae; Conus.			
OX	NCBI_TaxID=6491;			
RN	[1]			
RP	SEQUENCE, STRUCTURE BY NMR, SYNTHESIS, MASS SPECTROMETRY, AND			
RP	NOTAGNESIS OF ARG-12.			
RC	TISSUE=Venom;			
RX	PubMed=12419800; DOI=10.1074/jbc.M210280200;			
RA	Nicke A., Loughnan M.L., Millard E.L., Alewood P.F., Adams D.J.,			
RA	Daly N.L., Craik D.J., Lewis R.J.,			
RT	"Isolation, structure, and activity of GID, a novel alpha 4/7-			
RT	conotoxin with an extended N-terminal sequence."			
RL	J. Biol. Chem. 278:3137-3144(2003).			
CC	-1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they			
CC	bind to the nicotinic acetylcholine receptors (nAChR) and thus			
CC	inhibit them. This peptide reversibly inhibits alpha-7, alpha-			
CC	3/beta-2, and alpha-4/beta-2 subunits.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: Expressed by the venom duct.			
CC	-1- MASS SPECTROMETRY: MW=2184.9; RANGE=1-19; NOTED=Ref.1.			
CC	-1- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type			
CC	family.			
DR	PDB; 1MTQ; NMR; "			
KM	3D-structure: Acetylcholine receptor inhibitor;			
KM	Direct protein sequencing; Gamma-carboxyglutamic acid; Hydroxylation;			
KW	Neurotoxin; Postsynaptic neurotoxin; Toxin; Vitamin K.			
FT	DISULFID	5	11	
FT	MOD RES	6	19	
FT	MOD RES	4	4	
FT	MOD RES	16	16	
FT	MUTAGEN	12	12	
FT	MUTAGEN	1	4	
SQ	SEQUENCE	19 AA; 2130 MW;		
QY	Query Match	25.7%; Score 35; DB 1; Length 19;		
QY	Best Local Similarity	62.5%; Pred. No. 6.3e+02;		
QY	Matches	5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;		
QY	1 CRVTHPL 8			
QY	: :			
QY	11 CRVTHPLV 18			

RESULT 2

Q6TMS4 ID Q6TMS4 PRELIMINARY; PRT; 23 AA.
 AC Q6TMS4
 DT 05-JUN-2004 (TREMBlrel. 27, Created)
 DT 05-JUN-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUN-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=PSC12.5.424.9;
 OS Streptomyces clavuligerus.
 OG Plasmid PSC12.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycetales; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1901;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wu W., Roy K.L.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY392415; AAC93549.1; -.
 KM Hypothetical protein; Plasmid.
 SQ SEQUENCE 23 AA; 2374 MW; 6F371429BF49D3F8 CRC64;

Query Match 24.3%; Score 33; DB 2; Length 23;
 Best Local Similarity 40.0%; Pred. No. 1.5e+03;
 Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVERSI 16
 DB 8 QVANATLPRDLARHL 22

RESULT 3

CTIC_LITCI ID CTIC_LITCI STANDARD; PRT; 18 AA.
 AC P81844;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Cytropin 1.2.4.
 OS Litorea citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodytidae; Litorea.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA MEDLINE=99435977; PubMed=10504394;
 RA Wegener K.L., Wabnitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,
 RA Wallace J.C., Tyler M.J.;
 RT "Host defence peptides from the skin glands of the Australian blue
 RT ant bacterial peptide citropin 1.1.",
 RL Eur. J. Biochem. 265:627-637(1999).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Dorsal and subventral skin glands.
 KW Amphibian defense peptide; Direct protein sequencing.
 SQ SEQUENCE 18 AA; 1814 MW; 500BF778D515ABD7 CRC64;

Query Match 22.8%; Score 31; DB 1; Length 18;
 Best Local Similarity 33.3%; Pred. No. 2.3e+03;
 Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 11 DIVRSIAKAPGRAP 25
 DB 4 DITKVASVGLASP 18

RESULT 4

Q9BQTO ID Q9BQTO PRELIMINARY; PRT; 18 AA.

Q9BQTO; AC Q9BQTO;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21195339; PubMed=11297743; DOI=10.1016/S0014-5793(01)02318-3;
 RA Holmann K., Ambrosch I., Eibling U., Mische M., Berger W.;
 RT "A small upstream open reading frame causes inhibition of human major
 RT vault protein expression from a ubiquitous mRNA splice variant.",
 RL FEBS Lett. 494:99-104(2001).
 DR EMBL; AJ291367; CAC35315.1; -.
 KM Hypothetical protein.
 SQ SEQUENCE 18 AA; 2179 MW; 5D06F9A3F11CB828 CRC64;

Query Match 22.1%; Score 30; DB 2; Length 18;
 Best Local Similarity 66.7%; Pred. No. 3.3e+03;
 Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 CRVTHPHLP 9
 DB 8 CRL--PHLP 14

RESULT 5

Q9ORH8 ID Q9ORH8 PRELIMINARY; PRT; 19 AA.
 AC Q9ORH8;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Tat protein (Fragment).
 GN Name-tat;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=56C932.
 RX MEDLINE=2166216; PubMed=11804559; DOI=10.1089/089922202753394745;
 RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
 RA N'Doundou N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,
 RA Ido E., Hayami M., Ichimura H., Parra H. Joseph.,
 RT "Genetic subtypes of HIV type 1 based on the vpu/env sequences in the
 RT Republic of Congo.",
 RL AIDS Res. Hum. Retroviruses 18:79-83(2002).
 DR EMBL; AF127545; AAK84896.1; -.
 FT NON_TER 1 19
 FT NON_TER 1 19
 SQ SEQUENCE 19 AA; 2210 MW; 2A83642B89068236 CRC64;

Query Match 22.1%; Score 30; DB 2; Length 19;
 Best Local Similarity 53.8%; Pred. No. 3.4e+03;
 Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 PHLPRDIVRSIAK 18
 DB 7 PHSSDHDHNSLIPK 19

RESULT 6

Q99JV2 ID Q99JV2 PRELIMINARY; PRT; 20 AA.
 AC Q99JV2;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RA Strausberg R.; TISSUE=Mammary tumor. C3;
 RU Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC005653; AA005653.1; -
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 20 AA; 223 MW; F203F6A80A7A0429 CRC64;
 Query Match 22.1%; Score 30; DB 2; Length 20;
 Best Local Similarity 70.0%; Pred. No. 3.6e+03;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 13 VRSIAKAPGK 22
 DB 1 VFSIAKAPGK 10
 RESULT 7
 09T2R0 PRELIMINARY; PRT; 16 AA.
 AC 09T2R0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Cytochrome-c reductase 14 kDa subunit (EC 1.10.2.2) (Fragment).
 OS Solanum tuberosum (Potato).
 OC Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94198758; PubMed=7764624;
 RA Braun H.P., Krutz V., Schmitz U.K.;
 RL Planta 193:99-106(1994).
 DR GO; GO:0008121; F:ubiquinol-cytochrome-c reductase activity; IEA.
 SQ SEQUENCE 16 AA; 1946 MW; BBC625F8B4A4C8E7 CRC64;
 Query Match 21.3%; Score 29; DB 2; Length 16;
 Best Local Similarity 50.0%; Pred. No. 4.1e+03;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 5 HPHLPKDI 12
 DB 2 HOYLPEDL 9
 RESULT 8
 CTIA_LITCI STANDARD; PRT; 18 AA.
 ID CTIA_LITCI
 AC P81838;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Citropin 1.1.3.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
 OC Pelodytidae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=94435977; PubMed=10504394;
 RA Weegner K.L., Mohlitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,
 Wallace J.C., Tyler M.J.;

RT "Host defence peptides from the skin glands of the Australian blue
 mountains tree-frog Litoria citropa. Solution structure of the
 RT antibacterial peptide citropin 1.1.";
 RL Eur. J. Biochem. 265:627-637(1999).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Dorsal and subventral skin glands.
 KW Amphibian defense peptide; Direct protein sequencing.
 SQ SEQUENCE 18 AA; 1814 MW; 500BF778D51F98D7 CRC64;
 Query Match 21.3%; Score 29; DB 1; Length 18;
 Best Local Similarity 26.7%; Pred. No. 4.6e+03;
 Matches 4; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 11 DIVRSIAKAPGKAP 25
 DB 4 DVIAKVASVIGLASP 18
 RESULT 9
 016271 PRELIMINARY; PRT; 19 AA.
 ID 016271;
 AC 016271;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Arginine vasopressin V2 receptor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95086168; PubMed=7993996;
 RA Holtzman E.J., Kolkowski L.F., Gelman-Holtzman O., O'Brien D.G.,
 RA Rasolampour M., Gulliot A.P., Ausiello D.A.;
 RT "Mutations in the vasopressin V2 receptor gene in two families with
 RT nephrogenic diabetes insipidus.";
 RL J. Am. Soc. Nephrol. 5:169-176(1994).
 DR EMBL; S75754; AAB3753.1; -
 DR GO; GO:0004872; F:receptor activity; IEA.
 FT NON TER 19
 SQ SEQUENCE 19 AA; 1905 MW; 181640BFD90F2788 CRC64;
 Query Match 21.3%; Score 29; DB 2; Length 19;
 Best Local Similarity 37.5%; Pred. No. 4.8e+03;
 Matches 6; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 QY 5 HPHLPKDI VRSIAKAP 20
 DB 4 HPSLPSCAMASLSAQF 19
 RESULT 10
 06A1F4 PRELIMINARY; PRT; 21 AA.
 ID 06A1F4;
 AC 06A1F4;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Multiple sugar metabolism regulator (Fragment).
 GN NameamR;
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ramachandran V., McArthur J.D., Behm C.E., Gutzelt C., Dowton M.,
 RA Fagan P.K., Towers R.J., Currie B.J., Sidprakash K.S., Walker M.J.;
 RT "Distribution and molecular evolution of the fibronectin binding
 RT protein prf2 gene family in Streptococcus pyogenes isolated from the
 RT Northern Territory of Australia.";

RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ784873; CAH04963.1; -.
 FT NON TER 21 21
 SQ SEQUENCE 21 AA; 2332 MW; 2086BDCA45FE51A1 CRC64;

Query Match 21.3%; Score 29; DB 2; Length 21;
 Best Local Similarity 45.5%; Pred. No. 5.4e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 PHLPKDIVR1 16
 |||:|:
 DB 5 PHFPINNVRL 15

RESULT 11
 H2B1_ECHES STANDARD; PRT; 25 AA.
 AC P13281;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Histone H2B.1, sperm (Fragment).
 OS Echinus esculentus (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoida; Euechinoidea; Echinacea; Echinoida; Echinidae; Echinus.
 NCBI_TaxID=7648;
 RX MEDLINE=90126812; Pubmed=2298202;
 RA Hall C.S., Thomas J.O.,
 RT "Core histone-DNA interactions in sea urchin sperm chromatin. The N-
 terminal tail of H2B interacts with linker DNA.",
 RL Eur. J. Biochem. 187:145-153(1990).
 CC -1- SUBUNIT: The nucleosome is an octamer containing two molecules
 of H2A, H2B, H3 and H4. The octamer wraps approximately 146
 bp of DNA.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: Belongs to the histone H2B family.
 DR PIR; S07770; S07770.
 DR InterPro; IPR000558; Histone H2B.
 DR PROSITE; PS00357; HISTONE_H2B; PARTIAL.
 KM Chromosomal protein; Direct protein sequencing; DNA-binding;
 KM Multigene family; Nuclear protein; Nucleosome core.
 FT NON TER 25 25
 SQ SEQUENCE 25 AA; 2693 MW; 9842DD3D73A3A9EC CRC64;

Query Match 21.3%; Score 29; DB 1; Length 25;
 Best Local Similarity 62.5%; Pred. No. 6.4e+03;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 18 KAFGRAP 25
 |||:|:
 DB 4 KSPTKRSP 11

RESULT 12
 Q7M374 PRELIMINARY; PRT; 11 AA.
 AC Q7M374;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Ribosomal protein MRP-S24, mitochondrial (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 NCBI_TaxID=9913;
 RX DOI=10.1101/110111; PubMed=10715014;
 RA Gordacheva V.Y., Godfrey H.P., Cabelli F.C.,
 RT "Analysis of the bmp gene family in *Borrelia burgdorferi sensu lato*.",
 DR EMBL; AF222435; AAF45174.1; -.
 FT NON TER 1 1
 SQ SEQUENCE 11 AA; 1161 MW; 57F3887CD59126F9 CRC64;
 RA Grack H.R.,
 DR Submitted (JUL-1999) to the PIR data bank.
 PIR; S78765; S78765.

FT NON TER 1 1
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1264 MW; 95F49156A32772CA CRC64;

Query Match 20.6%; Score 28; DB 2; Length 11;
 Best Local Similarity 40.0%; Pred. No. 3.9e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 HPPLPKDIVR 14
 |||:|:
 DB 2 HVDVPRDLTK 11

RESULT 13
 Q9MX47 PRELIMINARY; PRT; 22 AA.
 AC Q9MX47;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN Name=Oria-DCB;
 OS Oryzias latipes (Medaka fish) (Japanese ricefish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorphi; Atherinomorpha;
 OC Belontiiformes; Adiantichthyidae; Oryziatidae; Oryzias.
 NCBI_TaxID=8090;
 RX MEDLINE=8090;
 RA Naruse K., Oka H., Kojima A., Beseho Y., Kuroda N., Matsuzaki T.,
 RT "Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases."
 RL EMBL; AB031216; BAA94283.1; -.
 FT NON TER 22 22
 SQ SEQUENCE 22 AA; 2441 MW; E2AP1A9CD581F5FB CRC64;

Query Match 20.6%; Score 28; DB 2; Length 22;
 Best Local Similarity 38.5%; Pred. No. 7.9e+03;
 Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 CRVTHPHPKDIV 13
 |||:|:
 DB 7 CRVTHVSLKDP1 19

RESULT 14
 Q9L7N8 PRELIMINARY; PRT; 24 AA.
 AC Q9L7N8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Bmpd (Fragment).
 GN Name=bmpd;
 OS *Borrelia afzelii*.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
 NCBI_TaxID=29518;
 RX DOI=10.1101/110111; PubMed=10715014;
 RA Gordacheva V.Y., Godfrey H.P., Cabelli F.C.,
 RT "Analysis of the bmp gene family in *Borrelia burgdorferi sensu lato*.",
 DR EMBL; AF222435; AAF45174.1; -.
 FT NON TER 1 1
 SQ SEQUENCE 24 AA; 2681 MW; 57F3887CD59126F9 CRC64;
 Query Match 20.6%; Score 28; DB 2; Length 24;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 07:01.10 / Search time 161 Seconds
(without alignments)
60.056 Million cell updates/sec

Title: US-10-751-743-4

Perfect score: 136
Sequence: 1 CRVTHPLPKDIVRSIAKAPKAP 25

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 768190

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: A_Geneseq.16Dec04:*
2: geneseqp19808:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	75.0	20	AAW24102	AAW24102 Canine im
2	89	65.4	17	AAV50894	AAV50894 Antibody
3	89	65.4	17	AAV50893	AAV50893 Antibody
4	89	65.4	17	ADQ76003	ADQ76003 Peptide c
5	89	65.4	25	AAV79999	AAV79999 Optimised
6	79	58.1	20	AAW24103	AAW24103 Canine im
7	72	52.9	17	AAV50896	AAV50896 Antibody
8	72	52.9	17	ADQ76005	ADQ76005 Peptide c
9	69	50.7	17	AAV50895	AAV50895 Antibody
10	69	50.7	17	ADQ76004	ADQ76004 Peptide c
11	68	50.0	25	AAV80000	AAV80000 Optimised
12	65	47.8	17	AAV50898	AAV50898 Antibody
13	65	47.8	17	ADQ76007	ADQ76007 Peptide c
14	64	47.1	25	AAV68602	AAV68602 Peptide s
15	64	47.1	25	AAV91212	AAV91212 Modified
16	64	47.1	25	AAV79998	AAV79998 Optimised
17	63	46.3	25	AAV80077	AAV80077 Optimised
18	61	44.9	17	AAV50897	AAV50897 Antibody
19	61	44.9	17	ADQ76006	ADQ76006 Peptide c
20	60	44.1	14	AAO18028	AAO18028 Human imm
21	60	44.1	14	ABU00529	ABU00529 Human IGE
22	60	44.1	16	AAO18018	AAO18018 Human imm
23	60	44.1	16	AAO18041	AAO18041 Human imm
24	60	44.1	16	ADG17011	ADG17011 Human imm
25	60	44.1	16	ADG17005	ADG17005 Human imm

26	60	44.1	17	ADG17049	ADG17049 Disulphid
27	60	44.1	18	AAO18030	AAO18030 Human imm
28	60	44.1	18	AAO18039	AAO18039 Human imm
29	60	44.1	18	AAO18042	AAO18042 Human imm
30	60	44.1	18	AAO18036	AAO18036 Human imm
31	60	44.1	18	ABJ00531	ABJ00531 Human IGE
32	60	44.1	18	ABJ00537	ABJ00537 Human IGE
33	60	44.1	18	ADG17020	ADG17020 Human imm
34	60	44.1	18	ADG17006	ADG17006 Human imm
35	60	44.1	18	ADG17012	ADG17012 Human imm
36	60	44.1	18	ADG17014	ADG17014 Human imm
37	60	44.1	20	AAO18031	AAO18031 Human imm
38	60	44.1	20	AAO18037	AAO18037 Human imm
39	60	44.1	20	ABJ00532	ABJ00532 Human IGE
40	60	44.1	20	ABJ00538	ABJ00538 Human IGE
41	60	44.1	20	ADG17019	ADG17019 Human imm
42	60	44.1	20	ADG17013	ADG17013 Human imm
43	60	44.1	21	ADG17044	ADG17044 Human imm
44	60	44.1	21	ADG17026	ADG17026 Human imm
45	60	44.1	21	ADG17038	ADG17038 Human imm

ALIGNMENTS

RESULT 1	
AAW24102	AAW24102 standard; peptide, 20 AA.
ID	AAW24102,
XX	AC
XX	AAW24102,
DT	21-NOV-1997 (first entry)
XX	DE
XX	Canine Immunoglobulin E peptide 5.
XX	KM
XX	Immunoglobulin E, IGE; anti-canine IGE antibody; allergy; canine; dog.
XX	OS
XX	Canis familiaris.
XX	PN
XX	JP09169795-A.
XX	PD
XX	30-JUN-1997.
XX	XX
PF	22-DEC-1995; 95JP-00334381.
XX	XX
PR	22-DEC-1995; 95JP-00334381.
XX	XX
PA	(HITB) HITACHI CHEM CO LTD.
XX	XX
DR	WPI, 1997-389423/36.
DR	N-PSDB; AAT85651.
XX	XX
PT	Canine Immunoglobulin E peptide fragment and related DNA - useful for the preparation of anti-canine immunoglobulin E antibody.
XX	XX
PS	Claim 2, Page 9, 12pp; Japanese.
XX	XX
CC	AAW24098-106 are peptide fragments containing at least 5 continuous amino acids of the partial canine immunoglobulin E (IGE) protein shown in
CC	AAW24097. The peptides are used for the preparation of anti-canine IGE
CC	antibody. The anti-canine IGE antibody can be used for the diagnosis of
CC	canine allergies
XX	XX
SQ	Sequence 20 AA;
Query Match	75.0%; Score 102; DB 2; Length 20;
Best local similarity	100.0%; Pred. No. 1.7e-08;
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 CRVTHPLPKDIVRSIAKA 19
Db	2 CRVTHPLPKDIVRSIAKA 20

RESULT 2
AA50894
ID AA50894 standard; peptide, 17 AA.
XX
AC AA50894;
XX
DT 24-FEB-2000 (first entry)
XX
DE Antibody 15A.2 canine IgE binding epitope 1.
XX
KM Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
XX epitope; prophylaxis; treatment; mimotope.
XX
OS Synthetic.
XX
PN EP957111-A2.
XX
PD 17-NOV-1999.
XX
PF 09-APR-1999; 99EP-00107035.
XX
PR 09-APR-1998; 98US-00058331.
XX 30-MAR-1999; 99US-00281760.
XX
PA (IDEX-) IDEXX LAB INC.
XX
PI Lawton R, Mermer B, Francoeur G;
XX
DR WPI; 2000-040833/04.
XX
PT Binding proteins used for treatment or prophylaxis of canine allergy.
XX
PS Disclosure; Fig 7; 30pp; English.
XX
CC This invention describes a novel binding protein which specifically binds
CC to native canine free or B-cell bound IgE, and which doesn't bind to IgE
CC when the IgE is bound to mast cells. The peptide products of the
CC invention have anti-allergic activity. The antibodies bind to defined
CC epitopes on free or B-cell bound IgE molecules which have an important
CC role in allergic reaction. The specific binding proteins are used to
CC produce a pharmaceutical composition, preferably with a diluent, which
CC can be used for prophylaxis or treatment of canine allergy. AA50876-
CC Y50900 represent peptide mimotopes used in the method of the invention
SQ
Sequence 17 AA;
XX
Query Match 65.4%; Score 89; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRVTHPHLPKDIVRSI 16
DB 2 CRVTHPHLPKDIVRSI 17
XX
RESULT 3
AA50893
ID AA50893 standard; peptide, 17 AA.
XX
AC AA50893;
XX
DT 24-FEB-2000 (first entry)
XX
DE Antibody 15A.2 binding peptide 10 from PhdC7c phage display library.
XX
KM Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
XX epitope; prophylaxis; treatment; mimotope.
XX
OS Synthetic.
XX
PN EP957111-A2.
XX

PD 17-NOV-1999.
XX
PF 09-APR-1999; 99EP-00107035.
XX
PR 09-APR-1998; 98US-00058331.
XX 30-MAR-1999; 99US-00281760.
XX
PA (IDEX-) IDEXX LAB INC.
XX
PI Lawton R, Mermer B, Francoeur G;
XX
DR WPI; 2000-040833/04.
XX
PT Binding proteins used for treatment or prophylaxis of canine allergy.
XX
PS Disclosure; Fig 6; 30pp; English.
XX
CC This invention describes a novel binding protein which specifically binds
CC to native canine free or B-cell bound IgE, and which doesn't bind to IgE
CC when the IgE is bound to mast cells. The peptide products of the
CC invention have anti-allergic activity. The antibodies bind to defined
CC epitopes on free or B-cell bound IgE molecules which have an important
CC role in allergic reaction. The specific binding proteins are used to
CC produce a pharmaceutical composition, preferably with a diluent, which
CC can be used for prophylaxis or treatment of canine allergy. AA50876-
CC Y50900 represent peptide mimotopes used in the method of the invention
SQ
Sequence 17 AA;
XX
Query Match 65.4%; Score 89; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRVTHPHLPKDIVRSI 16
DB 2 CRVTHPHLPKDIVRSI 17
XX
RESULT 4
ADQ76003
ID ADQ76003 standard; peptide, 17 AA.
XX
AC ADQ76003;
XX
DT 07-OCT-2004 (first entry)
XX
DE Peptide capable of preventing IgE binding to high affinity receptor #2.
XX
KM allergy; allergic symptom; IgE binding.
XX
OS Synthetic.
XX
PN WO2004058799-A2.
XX
PD 15-JUL-2004.
XX
PE 19-DEC-2003; 2003WO-US040711.
XX
PR 20-DEC-2002; 2002US-00325375.
XX
PA (IDEX-) IDEXX LAB INC.
XX
PI Krah ER, Lawton R;
XX
DR WPI; 2004-534123/51.
XX
XX New isolated polypeptides and encoding polynucleotides, useful for
XX preventing and/or treating allergic diseases and allergy symptoms in
XX mammals.
XX
XX Claim 5; SEQ ID NO 2; 50pp; English.
XX
CC The present invention relates to isolated polypeptides capable of

CC inhibiting the binding of IGB to a high affinity receptor. These are
 CC useful for the prevention and/or treatment of allergic diseases and
 CC allergy symptoms in mammals. The present sequence is a polypeptide of the
 CC invention.

XX Sequence 17 AA;

Query Match 65.4%; Score 89; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRVTHPHLPKDIVRSI 16
 |||||
 Db 2 CRVTHPHLPKDIVRSI 17

RESULT 5
 AAY79999
 ID AAY79999 standard; peptide; 25 AA.
 XX
 AC AAY79999;
 XX
 DT 15-MAY-2000 (first entry)
 XX

Optimised IGB-CH3 domain antigen peptide for dog IGB.

XX Immunoglobulin B; IGB; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KM antibody; allergy; allergic disease; immunisation; anti-allergic;
 KM anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Canis sp.
 OS Synthetic.
 PN WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US013959.

XX 20-JUN-1998; 98US-00100287.

PA (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

PT New antigenic peptide from the CH3 domain of immunoglobulin B, fusions
 for immunization against allergy.

PS Claim 1; Page 99; 15pp; English.

XX The present invention describes immunoglobulin B (IGB)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for
 CC a target effector site on the epsilon-heavy chain of IGB, and so
 CC preventing triggering and activation of mast cells and basophils and
 CC downregulation of IGB synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IGB-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe (non-
 CC anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid
 CC sequences used in the exemplification of the present invention

XX Sequence 25 AA;

Query Match 65.4%; Score 89; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2.2e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RVTHPHLPKDIVRSIAK 18
 |||||
 Db 8 RVTHPHLPKDIVRSIAK 24

RESULT 6
 AAW24103
 ID AAW24103 standard; peptide; 20 AA.

XX AAW24103;

XX 21-NOV-1997 (first entry)

XX Canine immunoglobulin B peptide 6.

XX Immunoglobulin B; IGB; anti-canine IGB antibody; allergy; canine; dog.

XX Canis familiaris.

XX JP09169795-A.

XX 30-JUN-1997.

XX 22-DEC-1995; 95JP-00334381.

XX 22-DEC-1995; 95JP-00334381.

PA (HITB) HITACHI CHEM CO LTD.

XX WPI; 1997-389423/36.

XX N-PSDB; AAT85652.

PT Canine immunoglobulin B peptide fragment and related DNA - useful for the
 preparation of anti-canine immunoglobulin B antibody.

XX Claim 2; Page 9; 12pp; Japanese.

XX AAW24098-106 are peptide fragments containing at least 5 continuous amino
 CC acids of the partial canine immunoglobulin B (IGB) protein shown in
 CC AAW24097. The peptides are used for the preparation of anti-canine IGB
 CC antibody. The anti-canine IGB antibody can be used for the diagnosis of
 CC canine allergies

XX Sequence 20 AA;

Query Match 58.1%; Score 79; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.1e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KDIVRSIAKAPGRAP 25
 |||||
 Db 1 KDIVRSIAKAPGRAP 16

RESULT 7
 AAY50896
 ID AAY50896 standard; peptide; 17 AA.

XX AAY50896;

XX 24-FEB-2000 (first entry)

XX Antibody 15A.2 green monkey IGB binding epitope 1.

XX Canine; allergy; antibody 15A.2; IGB; B cell; mast cell; anti-allergy;
 KM epitope; prophylaxis; treatment; mimotope.

XX Synthetic.

```

XX CC The present invention relates to isolated polypeptides capable of
CC inhibiting the binding of IgB to a high affinity receptor. These are
CC useful for the prevention and/or treatment of allergic diseases and
CC allergy symptoms in mammals. The present sequence is a polypeptide of the
CC invention.
XX
SQ Sequence 17 AA;

Query Match 52.9%; Score 72; DB 8; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.00062;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0
QY 1 CRVTHPHLPKDIYRS 15
|||||: |||
2 CRVTHPHLPRIALYRS 16

RESULT 9
AAVS0895
ID AAVS0895 standard; peptide; 17 AA.
XX
AC AAVS0895;
XX
DT 24-FEB-2000 (first entry)
XX
DE Antibody 15A.2 human IgB binding epitope 1.
XX Canine; allergy; antibody 15A.2; IgB; B cell; mast cell; anti-allergy;
XX epitope; prophylaxis; treatment; mimotope.
XX Synthetic.
OS
XX EP957111-A2.
PN
XX 17-NOV-1999.
PD
XX
PF 09-APR-1999; 99EP-00107035.
XX
PR 09-APR-1998; 98US-00058331.
PR 30-MAR-1999; 99US-00281760.
XX
PA (IDEX-) IDEXX LAB INC.
XX
PI Lawton R, Mermer B, Francoeur G;
DR WPI; 2000-040833/04.
XX
PT Binding proteins used for treatment or prophylaxis of canine allergy.
XX
PS Disclosure; Flg 7; 30pp; English.
XX
CC This invention describes a novel binding protein which specifically binds
CC to native canine free or B-cell bound IgB, and which doesn't bind to IgE
CC when the IgB is bound to mast cells. The peptide products of the
CC invention have anti-allergic activity. The antibodies bind to defined
CC epitopes on free or B-cell bound IgB molecules which have an important
CC role in allergic reaction. The specific binding proteins are used to
CC produce a pharmaceutical composition, preferably with a diluent, which
CC can be used for prophylaxis or treatment of canine allergy. AAVS0876-
CC Y50900 represent peptide mimotopes used in the method of the invention
SQ
Sequence 17 AA;

Query Match 50.7%; Score 69; DB 3; Length 17;
Best Local Similarity 73.3%; Pred. No. 0.0018;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 CRVTHPHLPKDIYRS 15
|||||: |||
2 CRVTHPHLPRIALYRS 16
DB

```


XX Binding proteins used for treatment or prophylaxis of canine allergy.
 PT
 XX
 PS Disclosure; Fig 7; 30pp; English.

CC This invention describes a novel binding protein which specifically binds
 CC to native canine free or B-cell bound IGE, and which doesn't bind to IGE
 CC when the IGE is bound to mast cells. The peptide products of the
 CC invention have anti-allergic activity. The antibodies bind to defined
 CC epitopes on free or B-cell bound IGE molecules which have an important
 CC role in allergic reaction. The specific binding proteins are used to
 CC produce a pharmaceutical composition, preferably with a diluent, which
 CC can be used for prophylaxis or treatment of canine allergy. AAY50876-
 CC Y50900 represent peptide mimotopes used in the method of the invention
 XX
 SQ

Sequence 17 AA;

Query Match 47.8%; Score 65; DB 3; Length 17;
 Best Local Similarity 75.0%; Pred. No. 0.0075;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CRVTHPLPKDIVRSI 16
 Db 2 CAVTHPDLKPKIRSI 17

RESULT 13

ID ADQ76007 standard; peptide; 17 AA.

AC ADQ76007;

DT 07-OCT-2004 (first entry)

DE Peptide capable of preventing IGE binding to high affinity receptor #6.

KM allergy; allergic symptom; IGE binding.

OS Synthetic.

PN WO2004058799-A2.

PD 15-JUL-2004.

PF 19-DEC-2003; 2003WO-US040711.

PR 20-DEC-2002; 2002US-00325375.

PA (INDEX-) IDEXX LAB INC.

PI Krah ER, Lawton R;

DR WPI; 2004-534123/51.

PT New isolated polypeptides and encoding polynucleotides, useful for
 PT preventing and/or treating allergic diseases and allergy symptoms in
 PT mammals.

PS Claim 5; SEQ ID NO 6; 50pp; English.

CC The present invention relates to isolated polypeptides capable of
 CC inhibiting the binding of IGE to a high affinity receptor. These are
 CC useful for the prevention and/or treatment of allergic diseases and
 CC allergy symptoms in mammals. The present sequence is a polypeptide of the
 CC invention.
 CC
 XX

SQ Sequence 17 AA;

Query Match 47.8%; Score 65; DB 8; Length 17;
 Best Local Similarity 75.0%; Pred. No. 0.0075;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CRVTHPLPKDIVRSI 16

Db 2 CAVTHPDLKPKIRSI 17

RESULT 14

ID AAY68602 standard; peptide; 25 AA.

AC AAY68602;

DT 05-MAY-2000 (first entry)

DE Peptide sequence of the invention.

XX Helper T cell epitope; peptide immunogen; LHRH;
 KW luteinizing hormone-releasing hormone; spermatogenesis; ovulation;
 KW oestrus; sexual development; sex hormone; promiscuous T helper epitope;
 KW vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
 KW breast cancer; endometriosis; boar taint; meat quality; immunocastration.
 XX

OS Unidentified.

PN WO966952-A1.

PD 29-DEC-1999.

PF 21-JUN-1999; 99WO-US013960.

PR 20-JUN-1998; 98US-00100414.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY;

DR WPI; 2000-160562/14.

PT New peptide immunogen containing luteinizing hormone-releasing hormone
 PT antigen site and helper T cell epitope, for e.g. contraception and
 PT treatment of cancer.
 PT
 XX

PS Disclosure; Page 92; 102pp; English.

CC The specification describes peptide immunogens comprising a synthetic
 CC helper T cell (Th) epitope and a target antigen, luteinizing hormone-
 CC releasing hormone (LHRH). The peptide immunogens cause induction of a
 CC specific immune response to LHRH which is involved in regulation of
 CC spermatogenesis, ovulation, oestrus, sexual development and secretion of
 CC sex hormones. Provision of a promiscuous T helper epitope (which is
 CC functional in genetically diverse subjects) provides optimum
 CC immunogenicity to the B cell epitopes of the target antigen and thus high
 CC antibody titres against the target antigen. The peptide immunogens of the
 CC invention are used to vaccinate against mammalian LHRH, for use as
 CC (reversible) contraceptive; control of hormone-dependent tumours (cancer
 CC of prostate or breast, also endometriosis); to prevent boar taint (and
 CC improve meat quality) and for immunocastration. The present sequence
 CC appears in the specification
 XX

SQ Sequence 25 AA;

Query Match 47.1%; Score 64; DB 3; Length 25;
 Best Local Similarity 64.7%; Pred. No. 0.017;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RVTTHPLPKDIVRSIAK 18
 Db 8 RVTTHPLPKDIVRSIAK 24

RESULT 15

ID AAY91212 standard; peptide; 25 AA.

AC AAY91212;

XX 22-MAY-2000 (first entry)
 DT Modified human Igs CH3 domain, SEQ ID NO:92.
 XX
 DE Promiscuous T-cell epitope; measles virus P protein; MVF;
 XX hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KM interleukin-2 releasing hormone; IL2RH; contraceptive; anticancer;
 KM somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KM foot and mouth disease virus; immunoglobulin B; IgB; anti-allergic;
 KM Plasmodium falciparum; circumsporozoite; antimalarial; CERP;
 KM cholesterol ester transport protein; anti-arteriosclerotic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO966957-A2.
 XX
 PD 29-DEC-1999.
 XX
 XX 21-JUN-1999; 99MO-US013975.
 PF
 XX 20-JUN-1998; 98US-00100412.
 PR
 XX (UNBI-) UNITED BIOMEDICAL INC.
 XX
 XX Wang CY;
 PI
 DR WPI; 2000-160564/14.
 XX
 PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus.
 PS
 PS Example 6; Page 40; 123pp; English.
 XX
 CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CERP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and immunocastration)
 CC / for promoting the growth of animals; or for treating allergies or
 CC arteriosclerosis. Incorporation of a promiscuous Th (functional in
 CC genetically diverse subjects) into an immunogen improves capacity to
 CC induce a strong T helper cell-mediated immune response, resulting in
 CC production of antibodies against a target antigen. Th can replace carrier
 CC proteins and pathogen-derived T helper epitopes. Sequence AAY91121
 CC represents a promiscuous T helper epitope from the measles virus P (MVP)
 CC protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246
 CC represent synthetic Th epitopes based on the MVP Th epitope. Sequence
 CC AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV)
 CC surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes
 CC derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-
 CC Y91244 are antigenic peptides comprising an LHRH sequence joined to a
 CC promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide
 CC used in these LHRH antigenic peptides. AAY91200 is somatostatin, and
 CC AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th
 CC epitope. Somatostatin immunogens may be used to promote growth in
 CC livestock. AAY91208 is a human CD4-CDR2-like domain antigenic site, and
 CC AAY91209-Y90211 are MVP Th epitope/CD4 CDR2 antigenic peptides which may
 CC be used to prevent HIV infection of T cells. AAY90212 is a modified
 CC version of a human Igs (immunoglobulin B) CH3 domain, and AAY90213-Y90219
 CC are Th epitope/Igs CH3 antigenic peptides which may be used in the
 CC treatment of allergies. AAY91220 is a peptide derived from foot and mouth
 CC disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this
 CC peptide and a Th epitope. AAY91223 is a Plasmodium falciparum

CC circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS
 CC antigen and an MVP Th epitope and may be used in a malaria vaccine.
 CC AAY91228-Y91231 represent CERP-derived peptides and AAY91232-Y91241 are
 CC immunogens comprising a CERP peptide and a Th epitope which may be used
 CC to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247
 CC and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-
 CC Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVP Th and
 CC HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1
 CC vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory
 CC invasion protein epitope from Yersinia species, and hinge spacer peptide,
 CC both of which may optionally be used in the antigenic peptides of the
 CC invention
 XX

SO Sequence 25 AA;

Query Match 47.1%; Score 64; DB 3; Length 25;
 Best local Similarity 64.7%; Pred. No. 0.017;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTTHPLPRALMRSSTK 18
 |||||:::|
 Db 8 RVTTHPLPRALMRSSTK 24

Search completed: February 22, 2005, 07:16:58
 Job time : 163 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 07:20:07 ; Search time 128 Seconds
(without alignments)
63.914 Million cell updates/sec

Title: US-10-751-743-4

Perfect score: 136
Sequence: 1 CRVTHPHLPDVIKAKGKRAP 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 298948

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodaca/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodaca/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /cgn2_6/ptodaca/2/pubpaa/US06_PUBCOMB.pep:*
- 4: /cgn2_6/ptodaca/2/pubpaa/US07_NEW_PUB.pep:*
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- 9: /cgn2_6/ptodaca/2/pubpaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodaca/2/pubpaa/US09C_PUBCOMB.pep:*
- 11: /cgn2_6/ptodaca/2/pubpaa/US09C_PUBCOMB.pep:*
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- 14: /cgn2_6/ptodaca/2/pubpaa/US10C_PUBCOMB.pep:*
- 15: /cgn2_6/ptodaca/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodaca/2/pubpaa/US10C_PUBCOMB.pep:*
- 17: /cgn2_6/ptodaca/2/pubpaa/US10C_PUBCOMB.pep:*
- 18: /cgn2_6/ptodaca/2/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodaca/2/pubpaa/US11_NEW_PUB.pep:*
- 20: /cgn2_6/ptodaca/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	136	100.0	25	US-09-938-700-4	Sequence 4, Appl1
2	89	65.4	17	US-10-325-375A-2	Sequence 2, Appl1
3	72	52.9	17	US-10-325-375A-4	Sequence 4, Appl1
4	69	50.7	17	US-10-325-375A-3	Sequence 3, Appl1
5	65	47.8	17	US-10-325-375A-6	Sequence 6, Appl1
6	64	47.1	23	US-10-630-070-96	Sequence 96, Appl1
7	64	47.1	23	US-10-630-074-96	Sequence 96, Appl1
8	61	44.3	17	US-10-325-375A-5	Sequence 5, Appl1
9	61	44.1	14	US-10-304-443-107	Sequence 107, Appl1
10	60	44.1	14	US-10-362-527-313	Sequence 313, Appl1
11	60	44.1	14	US-10-415-389-20	Sequence 20, Appl1
12	60	44.1	16	US-10-304-443-97	Sequence 97, Appl1
13	60	44.1	16	US-10-304-443-120	Sequence 120, Appl1

14	60	44.1	16	US-10-415-389-10	Sequence 10, Appl1
15	60	44.1	16	US-10-415-389-33	Sequence 33, Appl1
16	60	44.1	18	US-10-304-443-98	Sequence 98, Appl1
17	60	44.1	18	US-10-304-443-109	Sequence 109, Appl1
18	60	44.1	18	US-10-304-443-115	Sequence 115, Appl1
19	60	44.1	18	US-10-304-443-121	Sequence 121, Appl1
20	60	44.1	18	US-10-362-527-315	Sequence 315, Appl1
21	60	44.1	18	US-10-362-527-321	Sequence 321, Appl1
22	60	44.1	18	US-10-415-389-11	Sequence 11, Appl1
23	60	44.1	18	US-10-415-389-22	Sequence 22, Appl1
24	60	44.1	18	US-10-415-389-28	Sequence 28, Appl1
25	60	44.1	18	US-10-304-443-34	Sequence 34, Appl1
26	60	44.1	20	US-10-304-443-110	Sequence 110, Appl1
27	60	44.1	20	US-10-304-443-116	Sequence 116, Appl1
28	60	44.1	20	US-10-362-527-316	Sequence 316, Appl1
29	60	44.1	20	US-10-362-527-322	Sequence 322, Appl1
30	60	44.1	20	US-10-415-389-23	Sequence 23, Appl1
31	60	44.1	20	US-10-415-389-29	Sequence 29, Appl1
32	60	44.1	25	US-09-974-449-33	Sequence 33, Appl1
33	56	41.2	14	US-10-304-443-96	Sequence 96, Appl1
34	56	41.2	14	US-10-304-443-119	Sequence 119, Appl1
35	56	41.2	14	US-10-415-389-9	Sequence 9, Appl1
36	56	41.2	14	US-10-415-389-32	Sequence 32, Appl1
37	56	41.2	16	US-10-304-443-108	Sequence 108, Appl1
38	56	41.2	16	US-10-304-443-114	Sequence 114, Appl1
39	56	41.2	16	US-10-362-527-314	Sequence 314, Appl1
40	56	41.2	16	US-10-362-527-320	Sequence 320, Appl1
41	56	41.2	16	US-10-415-389-21	Sequence 21, Appl1
42	56	41.2	16	US-10-415-389-27	Sequence 27, Appl1
43	56	40.4	19	US-10-322-210-3	Sequence 3, Appl1
44	55	40.4	19	US-10-304-443-3	Sequence 3, Appl1
45	55	40.4	19	US-10-362-527-62	Sequence 62, Appl1

ALIGNMENTS

RESULT 1
US-09-938-700-4
Sequence 4, Application US/09938700
Patent No. US2002064525A1
GENERAL INFORMATION:
APPLICANT: Morsey, et al.
TITLE OF INVENTION: Anti-IGB Vaccines
FILE REFERENCE: PCT0761A
CURRENT APPLICATION NUMBER: US/09/938, 700
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 25
TYPE: PRT
ORGANISM: DOG CH3/CH4 PEPTIDE SEQUENCE
US-09-938-700-4

Query Match 100.0%; Score 136; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 4, 6e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRVTHPHLPDVIKAKGKRAP 25
Db 1 CRVTHPHLPDVIKAKGKRAP 25

RESULT 2
US-10-325-375A-2
Sequence 2, Application US/10325375A
Publication No. US20030229021A1
GENERAL INFORMATION:
APPLICANT: IDEXX Laboratories, Inc.
APPLICANT: Kraich, Eugene R.
APPLICANT: Lawton, Robert
TITLE OF INVENTION: Methods and Compositions for Inhibiting Binding of Ige to a High

```

; TITLE OF INVENTION: Affinity Receptor
; FILE REFERENCE: MBHB-01-672-E
; CURRENT APPLICATION NUMBER: US/10/325,375A
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Isolated polypeptide that binds to Igb.
US-10-325-375A-2

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Query Match      65.4%; Score 89; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 CRVTHPHLPKDIVRSI 16
        |||||
Db      2 CRVTHPHLPKDIVRSI 17

```

```

RESULT 3
US-10-325-375A-4
; Sequence 4, Application US/10325375A
; Publication No. US20030229021A1
; GENERAL INFORMATION:
; APPLICANT: IDEXX Laboratories, Inc.
; APPLICANT: Krahn, Eugene R.
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Binding of Ige to a High
; FILE REFERENCE: MBHB-01-672-E
; CURRENT APPLICATION NUMBER: US/10/325,375A
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Isolated polypeptide that binds to Igb.
US-10-325-375A-4

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Query Match      52.9%; Score 72; DB 15; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.003;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY      1 CRVTHPHLPKDIVRS 15
        |||||
Db      2 CRVTHPHLPALVRS 16

```

```

RESULT 4
US-10-325-375A-3
; Sequence 3, Application US/10325375A
; Publication No. US20030229021A1
; GENERAL INFORMATION:
; APPLICANT: IDEXX Laboratories, Inc.
; APPLICANT: Krahn, Eugene R.
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Binding of Ige to a High
; FILE REFERENCE: MBHB-01-672-E
; CURRENT APPLICATION NUMBER: US/10/325,375A
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT

```

```

; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Isolated polypeptide that binds to Igb.
US-10-325-375A-3

```

```

Query Match      50.7%; Score 69; DB 15; Length 17;
Best Local Similarity 73.3%; Pred. No. 0.008;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY      1 CRVTHPHLPKDIVRS 15
        |||||
Db      2 CRVTHPHLPALVRS 16

```

```

RESULT 5
US-10-325-375A-6
; Sequence 6, Application US/10325375A
; Publication No. US20030229021A1
; GENERAL INFORMATION:
; APPLICANT: IDEXX Laboratories, Inc.
; APPLICANT: Krahn, Eugene R.
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Binding of Ige to a High
; FILE REFERENCE: MBHB-01-672-E
; CURRENT APPLICATION NUMBER: US/10/325,375A
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Isolated polypeptide that binds to Igb.
US-10-325-375A-6

```

```

Query Match      47.8%; Score 65; DB 15; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.029;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      1 CRVTHPHLPKDIVRSI 16
        |||||
Db      2 CNVTHPDLPKILRSI 17

```

```

RESULT 6
US-10-630-070-96
; Sequence 96, Application US/10630070
; Publication No. US20050025781A1
; GENERAL INFORMATION:
; APPLICANT: Millich, David R.
; APPLICANT: Billaud, Jean-Noel
; TITLE OF INVENTION: Rodent Hepatitis B Virus Core Proteins as Vaccine Platforms and
; FILE REFERENCE: VACCINE-07083
; CURRENT APPLICATION NUMBER: US/10/630,070
; CURRENT FILING DATE: 2003-07-30
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 96
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-630-070-96

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Query Match      47.1%; Score 64; DB 17; Length 23;
Best Local Similarity 64.7%; Pred. No. 0.056;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      2 RVTHPHLPKDIVRSIAK 18

```

Db 7 RVTHPHLPALMRSTTK 23

RESULT 7
US-10-630-074-96
; Sequence 96, Application US/10630074
; Publication No. US20050025782A1
; GENERAL INFORMATION:
; APPLICANT: Milich, David R.
; APPLICANT: Billaud, Jean-Noel
; TITLE OF INVENTION: Human Hepatitis B Virus Core Proteins as Vaccine Platforms and
; TITLE OF INVENTION: Methods of Use Thereof
; FILE REFERENCE: VACCINE-07971
; CURRENT APPLICATION NUMBER: US/10/630,074
; CURRENT FILING DATE: 2003-07-30
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 96
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-630-074-96

Query Match 47.1%; Score 64; DB 17; Length 23;
Best Local Similarity 64.7%; Pred. No. 0.056;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRSIAK 18
Db 7 RVTHPHLPALMRSTTK 23

RESULT 8
US-10-325-375A-5
; Sequence 5, Application US/10325375A
; Publication No. US20030229021A1
; GENERAL INFORMATION:
; APPLICANT: IDEXX Laboratories, Inc.
; APPLICANT: Krah, Eugene R.
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Binding of Ige to a High
; TITLE OF INVENTION: Affinity Receptor
; FILE REFERENCE: MBHB-01-672-B
; CURRENT APPLICATION NUMBER: US/10/325,375A
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Isolated polypeptide that binds to Igs.
US-10-325-375A-5

Query Match 44.9%; Score 61; DB 15; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.11;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIVRSI 16
Db 2 CKVTHPDLPLVIVRSI 17

RESULT 9
US-10-304-443-107
; Sequence 107, Application US/10304443
; Publication No. US20030170229A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Biologicals s.a.

APPLICANT: Peptide Therapeutics Ltd.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45173CIP
; CURRENT APPLICATION NUMBER: US/10/304,443
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US/09/698,906A
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Human peptide sequence
US-10-304-443-107

Query Match 44.1%; Score 60; DB 14; Length 14;
Best Local Similarity 69.2%; Pred. No. 0.12;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIV 13
Db 1 CRVTHPHLPALM 13

RESULT 10
US-10-362-527-313
; Sequence 313, Application US/10362527
; Publication No. US20040030106A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Mason, Sean
; APPLICANT: Turnell, William Gordon
; APPLICANT: Vinals Y De Basols, Carlotia
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
; FILE REFERENCE: B45236
; CURRENT APPLICATION NUMBER: US/10/362,527
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/EP01/09576
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: GB 0020717.5
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial variant of Homo sapiens Igs peptide
US-10-362-527-313

Query Match 44.1%; Score 60; DB 15; Length 14;
Best Local Similarity 69.2%; Pred. No. 0.12;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIV 13
Db 1 CRVTHPHLPALM 13

RESULT 11
US-10-415-389-20
; Sequence 20, Application US/10415389
; Publication No. US20040115220A1
; GENERAL INFORMATION:
; APPLICANT: De Basols, Carlotia Vinals Y
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45251
; CURRENT APPLICATION NUMBER: US/10/415,389
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: PCT/EP01/12932
; PRIOR FILING DATE: 2001-10-24

```
; PRIOR APPLICATION NUMBER: GB 0026334.3
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human IGE peptide mimotope
US-10-415-389-20
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```
Query Match          44.1%; Score 60; DB 16; Length 14;
Best Local Similarity 69.2%; Pred. No. 0.12;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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QY 1 CRVTHPLPKDIYV 13
Db 1 CRVTHPLPKALM 13
```

```
RESULT 12
; Sequence 97, Application US/10304443
; Publication No. US20030170229A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Biologicals s.a.
; APPLICANT: Peptide Therapeutics Ltd.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45173CTP
; CURRENT APPLICATION NUMBER: US/10/304,443
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US/09/698,906A
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 97
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human peptide sequence
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (2)
; OTHER INFORMATION: Where Xaa represents any 1 of 20 naturally occurring amino acids
US-10-304-443-97
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```
Query Match          44.1%; Score 60; DB 14; Length 16;
Best Local Similarity 71.4%; Pred. No. 0.14;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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QY 2 RVTTHPLPKDIYVS 15
Db 3 RVTTHPLPKALMRS 16
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```
RESULT 13
; Sequence 120, Application US/10304443
; Publication No. US20030170229A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Biologicals s.a.
; APPLICANT: Peptide Therapeutics Ltd.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45173CTP
; CURRENT APPLICATION NUMBER: US/10/304,443
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US/09/698,906A
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 120
; LENGTH: 16
; TYPE: PRT
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; ORGANISM: Human peptide sequence
US-10-304-443-120
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Query Match          44.1%; Score 60; DB 14; Length 16;
Best Local Similarity 71.4%; Pred. No. 0.14;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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```
QY 2 RVTTHPLPKDIYVS 15
Db 3 RVTTHPLPKALMRS 16
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```
RESULT 14
; Sequence 10, Application US/10415389
; Publication No. US20040115220A1
; GENERAL INFORMATION:
; APPLICANT: De Babols, Carlota Vinals Y
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45251
; CURRENT APPLICATION NUMBER: US/10/415,389
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: PCT/EP01/12932
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: GB 0026334.3
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human IGE peptide mimotope
; NAME/KEY: VARIANT
; LOCATION: (1)...(16)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-415-389-10
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Query Match          44.1%; Score 60; DB 16; Length 16;
Best Local Similarity 71.4%; Pred. No. 0.14;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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```
QY 2 RVTTHPLPKDIYVS 15
Db 3 RVTTHPLPKALMRS 16
```

```
RESULT 15
; Sequence 33, Application US/10415389
; Publication No. US20040115220A1
; GENERAL INFORMATION:
; APPLICANT: De Babols, Carlota Vinals Y
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45251
; CURRENT APPLICATION NUMBER: US/10/415,389
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: PCT/EP01/12932
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: GB 0026334.3
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human IGE peptide mimotope
US-10-415-389-33
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Query Match 44.1%; Score 60; DB 16; Length 16;
 Best Local Similarity 71.4%; Pred. No. 0.14;
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRS 15
 |||||: :|||
 Db 3 RVTHPHLPALMRS 16

Search completed: February 22, 2005, 07:32:24
 Job time : 128 secs

inis Page Blank (uspto)

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OM protein - protein search, using sw model

Run on: February 22, 2005, 07:14:16 ; Search time 44 Seconds
(without alignments)
42.414 Million cell updates/sec

Title: US-10-751-743-4

Perfect score: 136
Sequence: 1 CRVTHPLPRDIYRSIAKGRKAP 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 218077

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	65.4	17	4	US-09-281-760B-26
2	89	65.4	25	4	US-09-701-623C-6
3	89	65.4	17	4	US-09-281-760B-28
4	69	50.7	17	4	US-09-281-760B-27
5	68	50.0	25	4	US-09-701-623C-7
6	65	47.8	17	4	US-09-281-760B-30
7	64	47.1	25	3	US-09-100-414B-95
8	64	47.1	25	3	US-09-303-323-95
9	64	47.1	25	4	US-09-770-014-95
10	64	47.1	25	4	US-09-701-588C-92
11	64	47.1	25	4	US-09-701-623C-5
12	63	46.3	25	4	US-09-701-623C-84
13	61	44.9	17	4	US-09-281-760B-29
14	60	44.1	22	2	US-08-232-539D-19
15	60	44.1	24	2	US-08-232-539D-20
16	46	33.8	25	4	US-09-701-623C-55
17	42	30.9	25	4	US-09-281-760B-32
18	41	30.1	15	4	US-09-701-623C-8
19	40	29.4	15	4	US-09-281-760B-31
20	39	28.7	9	4	US-09-281-760B-18
21	39	28.7	9	4	US-09-281-760B-25
22	39	28.7	14	4	US-09-281-760B-10
23	36	26.5	18	2	US-09-017-205-52
24	36	26.5	22	2	US-08-455-079-18
25	36	26.5	23	2	US-08-455-079-14
26	35.5	26.1	22	1	US-07-988-925-12
27	35.5	26.1	22	2	US-08-362-780-12

28	35.5	26.1	22	4	US-09-563-222C-105	Sequence 105, App
29	35.5	26.1	22	4	US-08-478-684G-12	Sequence 12, App1
30	35	25.7	22	3	US-09-046-985-4	Sequence 4, App1
31	35	25.7	22	3	US-09-474-743-4	Sequence 4, App1
32	35	25.7	22	3	US-08-851-843A-208	Sequence 208, App
33	35	25.7	23	3	US-08-974-549A-327	Sequence 327, App
34	35	25.7	23	3	US-08-854-050-208	Sequence 208, App
35	35	25.7	23	3	US-09-430-323-208	Sequence 327, App
36	35	25.7	23	4	US-09-402-181B-327	Sequence 327, App
37	35	25.7	23	4	US-09-721-456-327	Sequence 327, App
38	34	25.0	12	2	US-08-323-686-15	Sequence 15, App1
39	34	25.0	21	2	US-08-480-190-80	Sequence 80, App1
40	34	25.0	21	2	US-08-488-379-80	Sequence 80, App1
41	34	25.0	21	4	US-08-475-399A-80	Sequence 80, App1
42	34	25.0	21	4	US-08-077-255A-80	Sequence 80, App1
43	34	25.0	21	5	PCT-US93-07545-80	Sequence 80, App1
44	33.5	24.6	20	4	US-08-861-153A-5	Sequence 5, App1
45	33	24.3	18	4	US-09-493-795B-79	Sequence 79, App1

ALIGNMENTS

```
RESULT 1
US-09-281-760B-26
; Sequence 26, Application US/09281760B
; Patent No. 6734287
; GENERAL INFORMATION:
; APPLICANT: Lawton, Robert
; APPLICANT: Mermet, Brian
; TITLE OF INVENTION: Specific Binding Protein for Treating
; TITLE OF INVENTION: Canine Allergy
; FILE REFERENCE: 01-1275A
; CURRENT APPLICATION NUMBER: US/09/281, 760B
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 09/058, 331
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatsSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-281-760B-26

Query Match      65.4% Score 89; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 CRVTHPLPRDIYRSI 16
      |||||
Db      2 CRVTHPLPRDIYRSI 17

RESULT 2
US-09-701-623C-6
; Sequence 6, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang P.D., Chang YI
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; TITLE OF INVENTION: ALLERGY
; FILE REFERENCE: 1151153US1
; CURRENT APPLICATION NUMBER: US/09/701, 623C
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100, 287
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
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/ LENGTH: 25
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-701-623C-6

Query Match 65.4%; Score 89; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRSIAK 18
Db 8 RVTHPHLPKDIVRSIAK 24

RESULT 3
US-09-281-760E-28
/ Sequence 28, Application US/09281760E
/ Patent No. 6734287
/ GENERAL INFORMATION:
/ APPLICANT: Lawton, Robert
/ APPLICANT: Mermet, Brion
/ APPLICANT: Francoeur, Greg
/ TITLE OF INVENTION: Specific Binding Protein for Treating
/ FILE REFERENCE: 01-1275A
/ CURRENT APPLICATION NUMBER: US/09/281,760E
/ PRIOR FILING DATE: 1999-03-30
/ PRIOR APPLICATION NUMBER: 09/058,331
/ PRIOR FILING DATE: 1998-04-09
/ NUMBER OF SEQ ID NOS: 39
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 28
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Cercopithecus aethiops
US-09-281-760E-28

Query Match 52.9%; Score 72; DB 4; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.0001;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPHLPDIVRS 15
Db 2 CRVTHPHLPALVRS 16

RESULT 4
US-09-281-760E-27
/ Sequence 27, Application US/09281760E
/ Patent No. 6734287
/ GENERAL INFORMATION:
/ APPLICANT: Lawton, Robert
/ APPLICANT: Mermet, Brion
/ APPLICANT: Francoeur, Greg
/ TITLE OF INVENTION: Specific Binding Protein for Treating
/ FILE REFERENCE: 01-1275A
/ CURRENT APPLICATION NUMBER: US/09/281,760E
/ PRIOR FILING DATE: 1999-03-30
/ PRIOR APPLICATION NUMBER: 09/058,331
/ PRIOR FILING DATE: 1998-04-09
/ NUMBER OF SEQ ID NOS: 39
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 27
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-281-760E-27

Query Match 50.7%; Score 69; DB 4; Length 17;
Best Local Similarity 73.3%; Pred. No. 0.00029;

Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 CRVTHPHLPDIVRS 15
Db 2 CRVTHPHLPALVRS 16

RESULT 5
US-09-701-623C-7
/ Sequence 7, Application US/09701623C
/ Patent No. 6811782
/ GENERAL INFORMATION:
/ APPLICANT: Wang Ph.D., Chang Yi
/ TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
/ FILE REFERENCE: 1151415U01
/ CURRENT APPLICATION NUMBER: US/09/701,623C
/ CURRENT FILING DATE: 2000-12-01
/ PRIOR APPLICATION NUMBER: PCT/US99/13959
/ PRIOR FILING DATE: 1999-06-21
/ PRIOR APPLICATION NUMBER: 09/100,287
/ PRIOR FILING DATE: 1998-06-20
/ NUMBER OF SEQ ID NOS: 91
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 7
/ LENGTH: 25
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-701-623C-7

Query Match 50.0%; Score 68; DB 4; Length 25;
Best Local Similarity 76.5%; Pred. No. 0.0006;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRSIAK 18
Db 8 RVDHHPFKDIVRSITK 24

RESULT 6
US-09-281-760E-30
/ Sequence 30, Application US/09281760E
/ Patent No. 6734287
/ GENERAL INFORMATION:
/ APPLICANT: Lawton, Robert
/ APPLICANT: Mermet, Brion
/ APPLICANT: Francoeur, Greg
/ TITLE OF INVENTION: Specific Binding Protein for Treating
/ FILE REFERENCE: 01-1275A
/ CURRENT APPLICATION NUMBER: US/09/281,760E
/ PRIOR FILING DATE: 1999-03-30
/ PRIOR APPLICATION NUMBER: 09/058,331
/ PRIOR FILING DATE: 1998-04-09
/ NUMBER OF SEQ ID NOS: 39
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 30
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Sus scrofa
US-09-281-760E-30

Query Match 47.8%; Score 65; DB 4; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.0013;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIVRSI 16
Db 2 CRVTHPHLPKDIVRSI 17

RESULT 7
US-09-100-414B-95
Sequence 95, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang Y1
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-95

Query Match 47.1%; Score 64; DB 3; Length 25;
Best Local Similarity 64.7%; Pred. No. 0.0028;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTTHPLPKDIVSIK 18
DB 8 RVTTHPLPKDIVSIK 24

RESULT 8
US-09-303-323-95
Sequence 95, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Y1
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-95

Query Match 47.1%; Score 64; DB 3; Length 25;
Best Local Similarity 64.7%; Pred. No. 0.0028;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTTHPLPKDIVSIK 18
DB 8 RVTTHPLPKDIVSIK 24

RESULT 9
US-09-770-014-95
Sequence 95, Application US/09770014
Patent No. 6559282
GENERAL INFORMATION:
APPLICANT: Wang, Chang Y1
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-770-014-95

Query Match 47.1%; Score 64; DB 4; Length 25;
Best Local Similarity 64.7%; Pred. No. 0.0026;

Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYTHPHLPKDIVRSIAK 18
| | | | | : : : : :
Db 8 RYTHPHLPALMRSTTK 24

RESULT 10

US-09-701-588C-92
; Sequence 92, Application US/09701588C
; Patent No. 6713301

GENERAL INFORMATION:

APPLICANT: UNITED BIOMEDICAL INC., ET AL.
TITLE OF INVENTION: ARTIFICIAL T HELPER CELL
EPITOPES AS IMMUNE STIMULATORS FOR SYNTHETIC
PEPTIDE IMMUNOGENS

NUMBER OF SEQUENCES: 151

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York

STATE: NY
COUNTRY: USA

ZIP: 10154-0054
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC Windows

SOFTWARE: Word 97

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/701,588C

FILING DATE: 29-Nov. 6713301-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/100,414

FILING DATE: 20-JUNE-1998

ATTORNEY/AGENT INFORMATION:

NAME: Maria H. Iain

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4158PCI

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-758-4800

TELEFAX: 212-751-6849

INFORMATION FOR SEQ ID NO: 92:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 92:

US-09-701-588C-92

Query Match 47.1%; Score 64; DB 4; Length 25;

Best Local Similarity 64.7%; Pred. No. 0.0028;

Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYTHPHLPKDIVRSIAK 18
| | | | | : : : : :
Db 8 RYTHPHLPALMRSTTK 24

RESULT 11

US-09-701-623C-5

; Sequence 5, Application US/09701623C

; Patent No. 6811782

GENERAL INFORMATION:

APPLICANT: Wang Ph.D., Chang Yi

TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF

ALLERGY

FILE REFERENCE: 11514153US1

CURRENT APPLICATION NUMBER: US/09/701,623C

CURRENT FILING DATE: 2000-12-01

PRIOR APPLICATION NUMBER: PCT/US99/13959

; PRIOR FILING DATE: 1999-06-21

; PRIOR APPLICATION NUMBER: 09/100,287

; PRIOR FILING DATE: 1998-06-20

; NUMBER OF SEQ ID NOS: 91

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 5

; LENGTH: 25

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-09-701-623C-5

Query Match 47.1%; Score 64; DB 4; Length 25;

Best Local Similarity 64.7%; Pred. No. 0.0028;

Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYTHPHLPKDIVRSIAK 18
| | | | | : : : : :
Db 8 RYTHPHLPALMRSTTK 24

RESULT 12

US-09-701-623C-84

; Sequence 84, Application US/09701623C

; Patent No. 6811782

GENERAL INFORMATION:

APPLICANT: Wang Ph.D., Chang Yi

TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF

ALLERGY

FILE REFERENCE: 11514153US1

CURRENT APPLICATION NUMBER: US/09/701,623C

CURRENT FILING DATE: 2000-12-01

PRIOR APPLICATION NUMBER: PCT/US99/13959

PRIOR FILING DATE: 1999-06-21

PRIOR APPLICATION NUMBER: 09/100,287

PRIOR FILING DATE: 1998-06-20

NUMBER OF SEQ ID NOS: 91

SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 84

; LENGTH: 25

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-09-701-623C-84

Query Match 46.3%; Score 63; DB 4; Length 25;

Best Local Similarity 68.8%; Pred. No. 0.004;

Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 YTHPHLPKDIVRSIAK 18
| : | | | | : : : : :
Db 9 VSHPDLPREVRSIAK 24

RESULT 13

US-09-281-760R-29

; Sequence 29, Application US/09281760R

; Patent No. 6734287

GENERAL INFORMATION:

APPLICANT: Lawton, Robert

APPLICANT: Weimer, Brian

APPLICANT: Francoeur, Greg

TITLE OF INVENTION: Specific Binding Protein for Treating

ALLERGY

FILE REFERENCE: 01-1275A

CURRENT APPLICATION NUMBER: US/09/281,760R

CURRENT FILING DATE: 1999-03-30

PRIOR APPLICATION NUMBER: 09/058,331

PRIOR FILING DATE: 1998-04-09

NUMBER OF SEQ ID NOS: 39

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 29
 LENGTH: 17
 TYPE: PRT
 ORGANISM: Felis catus
 US-09-281-7608-29

Query Match 44.1%; Score 61; DB 4; Length 17;
 Best Local Similarity 75.0%; Pred. No. 0.0053;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRVTHPHLPDIYRSI 16
 Db 2 CRVTHPHLPDIYRSI 17

RESULT 14
 US-08-232-539D-19
 Sequence 19, Application US/08232539D
 Patent No. 5965709
 GENERAL INFORMATION:
 APPLICANT: Presta, Leonard G.
 APPLICANT: Jardeu, Paula M.
 TITLE OF INVENTION: Ige Antagonists
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/232,539D
 FILING DATE: 21-Apr-1994
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/178583
 FILING DATE: 07-JAN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/744768
 FILING DATE: 14-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Svoboda, Craig G.
 REGISTRATION NUMBER: 39,044
 REFERENCE/DOCKET NUMBER: P0718P3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1489
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-232-539D-19

Query Match 44.1%; Score 60; DB 2; Length 22;
 Best Local Similarity 69.2%; Pred. No. 0.01;
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPHLPDIY 13
 Db 10 CRVTHPHLPALM 22

RESULT 15
 US-08-232-539D-20
 Sequence 20, Application US/08232539D
 Patent No. 5965709

GENERAL INFORMATION:
 APPLICANT: Presta, Leonard G.
 APPLICANT: Jardeu, Paula M.
 TITLE OF INVENTION: Ige Antagonists
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/232,539D
 FILING DATE: 21-Apr-1994
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/178583
 FILING DATE: 07-JAN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/744768
 FILING DATE: 14-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Svoboda, Craig G.
 REGISTRATION NUMBER: 39,044
 REFERENCE/DOCKET NUMBER: P0718P3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1489
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-232-539D-20

Query Match 44.1%; Score 60; DB 2; Length 24;
 Best Local Similarity 69.2%; Pred. No. 0.011;
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPHLPDIY 13
 Db 12 CRVTHPHLPALM 24

Search completed: February 22, 2005, 07:29:40
 Job time: 45 secs

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